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198134

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From: Jiang, Dong
Sent: Wednesday, August 09, 2006 5:52 PM
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Subject: 10/719,202

ETD = 716100

Please search residues 197-2218 of SEQ ID NO:1, and 2.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646
REM - 4D70
571-272-0872
Mail stop REM - 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____

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Qy	1	ATGCCTGTGTCTCTGGTTCTCTGTCTCTTGGCACTGGGCCGAAACCTGTGGTGGTCTCT	60
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Db	257	CTGGAGAGACTGATGAGCCTCAGGACATGCAAGCTGCTCTCTAGGCCCTCTCCTGCCAC	316
Qy	121	CTCTCGGATGGTGACCTGTCTGCCTCGCTTGGAGCCTCCAGTCTGCCCCAGGCCCTGTG	180
Db	317	CTCTCGGATGGTGACCTGTCTGCCTCGCTTGGAGCCTCCAGTCTGCCCCAGGCCCTGTG	376
Qy	181	CTAGTGCCTACCGCCTGCAGACGGAGCTGGTGCCTGAGGTGTCCACAGAGACAGATTGC	240
Db	377	CTAGTGCCTACCGCCTGCAGACGGAGCTGGTGCCTGAGGTGTCCACAGAGACAGATTGC	436

; APPLICANT: Burkhead, Steven K.									
; APPLICANT: Levin, Steven D.									
; APPLICANT: Kuestner, Rolf E.									
; APPLICANT: Gao, Zeren									
; APPLICANT: Jaspers, Stephen R.									
; APPLICANT: Bilsborough, Janine									
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14									
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN									
; TITLE OF INVENTION: INFLAMMATION									
; FILE REFERENCE: 04-06P1									
; CURRENT APPLICATION NUMBER: US/11/150,533									
; CURRENT FILING DATE: 2005-06-10									
; NUMBER OF SEQ ID NOS: 66									
; SOFTWARE: Fast-Seq for Windows Version 4.0									
; SEQ ID NO 25									
; LENGTH: 2269									
; TYPE: DNA									
; ORGANISM: Mus musculus									
US-11-150-533-25									
Query Match 97.9%; Score 1980.2; DB 16; Length 2269;									
Best Local Similarity 98.5%; Pred. No. 0;									
Matches 2019; Conservative 0; Mismatches 3; Indels 27; Gaps 1;									
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Qy	121	CTCTGGAGTGTGACGTGCTCTGCTGCTCGCTGGAAGCCTCAGTCTGCCAGGCCCTGTG	180						
Db	317	CTCTGGAGTGTGACGTGCTCTGCTGCTCGCTGGAAGCCTCAGTCTGCCAGGCCCTGTG	376						
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Db	377	CTAGTGCCTACCCGCTCGACAGGAGCTGGTGTGAGTGTGCACAGAACAGAGATTGC	436						
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Qy	301	GAAGCTGGAAGTCTGATTACAGAACTCCAGGAGCTAGGAAGCCTCTCTCCAGGCCCAG	360						
Db	497	GAAGCTGGAAGTCTGATTACAGAACTCCAGGAGCTAGGAAGCCTCTCTCCAGGCCCAG	556						
Qy	361	GTGGTGTCTCTCTTCCAGGCCCTACCCATCGCCCGCTGTGCCCTCTGAGAGTCCAGGTG	420						
Db	557	GTGGTGTCTCTCTTCCAGGCCCTACCCATCGCCCGCTGTGCCCTCTGAGAGTCCAGGTG	616						
Qy	421	CCCGCTGACCTGGTGCAGCTGGTCACTCCGTGGGTTCTGCCGATTTTACATGTTTCAG	480						
Db	617	CCCGCTGACCTGGTGCAGCTGGTCACTCCGTGGGTTCTGCCGATTTTACATGTTTCAG	676						
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Qy	574	AATGTCTTGTGACACTGGATGTCTCTGAGGACGAGACTTTTAGCTTCTTACTGTACCTG	633						
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Qy	634	CGTCCAGTCCCGGATGCTCTCAAACTCTTGTGTACAAAACTGTGACCTCAGAAC	693						
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Qy	1456	TACAGCGTCTGGTGGAGCACTGGCTCCGCGTTTGGCCAGATGCCACTCGCGTGGCC	1515	
Db	1697	TACAGCGTCTGGTGGAGCACTGGCTCCGCGTTTGGCCAGATGCCACTCGCGTGGCC	1756	
Qy	1516	GTGACCTGTGGAGCGCGCGAGCTGAGCGGCGACGAGCGCTTCCACAC	1575	
Db	1757	GTGACCTGTGGAGCGCGCGAGCTGAGCGGCGACGAGCGCTTCCACAC	1816	
Qy	1576	CAGGACCGCGTATCTTGGAGAGGTTGGCTGGTAACTCTTCTTCTTCCGCGCGCC	1635	
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Qy	1696	CTGCGCGCGCTGCTACGCTGGCTTACCGATTTCTTCAAGCGCGCGCGCGCGCGC	1755	
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Qy	1756	TACGTCGGGCTCTACTTCGACGGGCTGCTGCAACAGACTGTGCGCTCCGCTTCCG	1815	
Db	1997	TACGTCGGGCTCTACTTCGACGGGCTGCTGCAACAGACTGTGCGCTCCGCTTCCG	2056	
Qy	1816	GTGCGCGCGCTTCTTCCCTGCCAGCGAGCTGCGGCTTCTTGGATGCACTGCAGGGA	1875	
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Qy	1876	GGCTGCTCCACTTCCGCGGGCGACCCCGAGCCGGGTGGAGCGAGTGCACCGGCGCTG	1935	
Db	2117	GGCTGCTCCACTTCCGCGGGCGACCCCGAGCCGGGTGGAGCGAGTGCACCGGCGCTG	2176	
Qy	1936	CGGTCGGCGCTGACGCTGCTACTTCTAGCTCGGAAGCCCGAGGCTGCTGCGAGGAATGG	1995	
Db	2177	CGGTCGGCGCTGACGCTGCTACTTCTAGCTCGGAAGCCCGAGGCTGCTGCGAGGAATGG	2236	
Qy	1996	GACCTGGGACCTGCACTACACTAGAA	2022	
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; Sequence 4, Application US/09899471				
; Patent No. US20020146763A1				
; GENERAL INFORMATION:				
; APPLICANT: Gao, Zeren				
; TITLE OF INVENTION: Murine Cytokine Receptor				
; FILE REFERENCE: 00-46				
; CURRENT APPLICATION NUMBER: US/09/899,471				
; CURRENT FILING DATE: 2001-07-05				
; NUMBER OF SEQ ID NOS: 8				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 4				
; LENGTH: 2328				
; TYPE: DNA				
; ORGANISM: mouse				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (197)...(2290)				
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Best Local Similarity 96.6%; Pred. No. 0;				
Matches 2022; Conservative 0; Mismatches 0; Indels 72; Gaps 1;				
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Db	197	ATGCTCTGTCTGGTTCCTGCTTCTGGCACTGGGCGGAAACCCCTGTGCTCTCT	256	

Db	1337	GCTGACTCTTTGGGGCCCTTCAAGATGATATGCTGTAGTGGAGATGAATAACCGGCCTC	1396
Qy	1129	AACAACACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCCCAGCATGGCC	1188
Db	1397	AACAACACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCCCAGCATGGCC	1456
Qy	1189	TCCACGAGAGCTGCTCGCTCGGAGAGAGAGTGTCTGCAAGACTTCCGATCACACCAGTGT	1248
Db	1457	TCCACGAGAGCTGCTCGCTCGGAGAGAGAGTGTCTGCAAGACTTCCGATCACACCAGTGT	1516
Qy	1249	ATGCAGCTGTGGAACAGATGACAACTAGGATCGCTATGGGCGTGCCTCCCATGCAACAGTAC	1308
Db	1517	ATGCAGCTGTGGAACAGATGACAACTAGGATCGCTATGGGCGTGCCTCCCATGCAACAGTAC	1576
Qy	1309	ATCCACAGGCGCTGGGTCTTAGTATGCTGGCTGCTCTACTCTTTGGCTGCGGCGCTTTTC	1368
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Qy	1429	CTCTCCACTCCGCGCAGGAGCGGGCTACGAGCGTCTGCTGGGAGCACTGGCGGTCCGCG	1488
Db	1697	CTCTCCACTCCGCGCAGGAGCGGGCTACGAGCGTCTGCTGGGAGCACTGGCGGTCCGCG	1756
Qy	1489	TTGAGCCAGATGCCACTGCGCGTGGCCGCTGTGTGAGAGCGCCGCGAGCTGAGCGCG	1548
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Qy	1549	CACGGAGCCTTAGCTGGTTCCACCAACAGGAGCGCGTATCTTCGAGGAGGCTGGCGTG	1608
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Db	1937	ACAGTGAGCGCGGGCCGATGACGCCCTTCGCGCGCTGGCTCAGCTGCGTGTACCCGAT	1996
Qy	1729	TTCTCTGAAGCCGGGGCGACCGGCCGCTAGCTCGGGGTCTACTTCGACAGGGCTGCTGCAC	1788
Db	1997	TTCTCTGAAGCCGGGGCGACCGGCCGCTAGCTCGGGGTCTACTTCGACAGGGCTGCTGCAC	2056
Qy	1789	CCAGACTCTGTGCCCTCCCGCTTCGCGTTCGCGCCCGCTTCTCTCCCTGCCCCAGCAGCTG	1848
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Qy	1849	CCGGCTTTCTTGATGCACTGCAGGAGGCTGTCCACTTCGCGGGGGCGACCGCGGAC	1908
Db	2117	CCGGCTTTCTTGATGCACTGCAGGAGGCTGTCCACTTCGCGGGGGCGACCGCGGAC	2176
Qy	1909	CGGGTGAAACGAGTGACCAGGCGCTCGCGTTCGCGCCCTGAGCAGCTGTACTTCTAGCTCG	1968
Db	2177	CGGGTGAAACGAGTGAAACCGAGGCGCTCGCGTTCGCGCCCTGAGCAGCTGTACTTCTAGCTCG	2236
Qy	1969	GAAGCCCAAGCTGCTCGAGGAATGGAACTGGGACCTTCGCACTACACTAGAA	2022
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US-10-719-202-4
; Sequence 4, Application US/10719202
; Publication No. US20040121388A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10719.202

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; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197) ... (2290)
US-10-719-202-4

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Query Match	95.9%	Score 1940;	DB 8;	Length 2328;
Best Local Similarity	96.6%	Pred. No. 0;		

Qy	1	ATGCTGTGTCTCGGTTCTTGCTGTCTTGCGCACTGGGCGCGAAACCTGTGGTCTGTCTCT	60
Db	197	ATGCTGTGTCTCGGTTCTTGCTGTCTTGCGCACTGGGCGCGAAACCTGTGGTCTGTCTCT	256
Qy	61	CTGGAGAGACTGATGGAGCCTCAGGACACTGCGCTGCTCTCTAGGCTCTCTCTGCGCAC	120
Db	257	CTGGAGAGACTGATGGAGCCTCAGGACACTGCGCTGCTCTCTAGGCTCTCTCTGCGCAC	316
Qy	121	CTCTGGGATGGTGA CGTGTCTTGCTCTGCTCTGGAAGCCTCCAGTCTGCCCAGGCGCTGTG	180
Db	317	CTCTGGGATGGTGA CGTGTCTTGCTCTGCTCTGGAAGCCTCCAGTCTGCCCAGGCGCTGTG	376
Qy	181	CTAGTGCTACCCGCTTG CAGACGGAGCTGGTGTCTAGAGTGTCCACAGAGA CAGATTGC	240
Db	377	CTAGTGCTACCCGCTTG CAGACGGAGCTGGTGTCTAGAGTGTCCACAGAGA CAGATTGC	436
Qy	241	GCCTCCGTCGCTCGTGTGGTGGTCCACTTGGCCGTGCA TGGGCACTGGGCAGAGCCTGAA	300
Db	437	GCCTCCGTCGCTGTGTGGTGGTCCACTTGGCCGTGCA TGGGCACTGGGCAGAGCCTGAA	496
Qy	301	GAAGCTGGAAAGTCTGA TTCAGAACTCCAGGAGTCTTAGGAA CGGCTCTCTCCAGGCGCAG	360
Db	497	GAAGCTGGAAAGTCTGA TTCAGAACTCCAGGAGTCTTAGGAA CGGCTCTCTCCAGGCGCAG	556
Qy	361	GTGGTGCTCTCCCTTCCAGAGGCTACCCCATCGCCGCTGCGCTCTGCTGGAGGTCCAGGTG	420
Db	557	GTGGTGCTCTCCCTTCCAGAGGCTACCCCATCGCCGCTGCGCTCTGCTGGAGGTCCAGGTG	616
Qy	421	CCGCTGACCTGGTG CAGCCTGGTCTAGCTCGCTGGGTTCTCGGTA TTTGACTGTTTCGAG	480
Db	617	CCGCTGACCTGGTG CAGCCTGGTCTAGCTCGCTGGGTTCTCGGTA TTTGACTGTTTCGAG	676
Qy	481	GCTAGTCTTGGGGCTGAGGTTACAGATCTGCTCTACAGAA GCGCAGGTACCGAAGAG	540
Db	677	GCTAGTCTTGGGGCTGAGGTTACAGATCTGCTCTACAGAA GCGCAGGTACCGAAGAG	736
Qy	541	CTCAACTCACAGCAGCTGGCTT-----	564
Db	737	CTCAACTCACAGCAGCTGGCTT-----	796
Qy	565	-----GATGGTGA CAATGCTCTTGACATGCTCTTGACA	588
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Db	857	CTGGATGTCTTGAGGAGCAGGACTTTAGCTTCTTACTGTA CTGCGTCAAGTCCCGGAT	916
Qy	649	GCTCTCAAAATCCTTGTGTACAAAACCTCACTGGACCTCAGAACTTACTTTAAACCAAC	708
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[illegible]

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QY 589 CTGGATGTCTTGAGGAGAGAGACTTTAGCTTTCTTACTGTACTGCTGCTCAGTCCCGAT 648
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DB 1381 ATCCACAGCGCTGGGTCTAGTATGCTGGCTGCTGCTTCTTGGCTGCGGCGCTTTTC 1440
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DB 1801 TTCTCTCAAGGCGCGCGCGCACCGCGCTACCTCGGGGTCTACTTCGACGGGCTGCTGCAC 1860
QY 1789 CCAGACTCTGTCCTTCCGCTTCCGCGTCCCGCTTCTTCTCCCTGCCCAAGCAGCTG 1848
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QY 1969 GAAGCCCCAGGCTCTGCGAGGAATGGAGCTGGGACCTTGACACTACACTAGAA 2022
DB 2041 GAAGCCCCAGGCTCTGCGAGGAATGGAGCTGGGACCTTGACACTACACTAGAA 2094

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US-10-152-661-487
; Sequence 487, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krihanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c5
; CURRENT APPLICATION NUMBER: US/10/152,661
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/866,050
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/221,232
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/206,650
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/312,283
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 09/188,930
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: 09/069,726
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-487

Query Match	95.6%	Score 1933.6	DB 6	Length 2128
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61	CTGGAGAGCTGATGAGGCTCAGGACATGACACCTGCTCTCTAGGCTCTCTCTGCGAC	120		
61	CTGGAGAGCTGATGAGGCTCAGGACATGACACCTGCTCTCTAGGCTCTCTCTGCGAC	120		
121	CTCTGGAGTGGTGAACGTCCTGTCCTTGGAGCTTCCAGTCTGCCCCCAGGCCCTGTG	180		
121	CTCTGGAGTGGTGAACGTCCTGTCCTTGGAGCTTCCAGTCTGCCCCCAGGCCCTGTG	180		
181	CTAGTGCCTACCCGCTGACAGCGAGCTGCTGAGGTGTCCACAGAGACAGATTGC	240		
181	CTAGTGCCTACCCGCTGACAGCGAGCTGCTGAGGTGTCCACAGAGACAGATTGC	240		
241	GCCCTCGGTCTCGTGTGGTGTCCATTGGCCGTGATGGGCACTGGGACAGGCTGAA	300		
241	GCCCTCGGTCTCGTGTGGTGTCCATTGGCCGTGATGGGCACTGGGACAGGCTGAA	300		
301	GAAGCTGGAAGTCTGATTCAAGAACTCCAGAGTCTAGGAACGCTCTCTCAGAGCCAG	360		
301	GAAGCTGGAAGTCTGATTCAAGAACTCCAGAGTCTAGGAACGCTCTCTCAGAGCCAG	360		
361	GTGTGTCTCTCTTCCAGGCTTACCCATGCGCCGTGCTGCTGCTGAGGCTCAGAGTG	420		
361	GTGTGTCTCTCTTCCAGGCTTACCCATGCGCCGTGCTGCTGCTGAGGCTCAGAGTG	420		
421	CCCGCTGACTCGTGTGAGCTGCTGCTGAGTCTCGTGGTTCCTGGGTATTGACTGTTGAG	480		
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481	GCTAGTCTTGGGGCTGAGGTAAGATCTGGTCTTACAGAGGCCAGGTAACAGAAAGAG	540		
541	CTCAACCTCACAGCAGCTGCTT-----GATGTGCAAAATGCTCTCTGACA	588		
541	CTCAACCTCACAGCAGCTGCTT-----GATGTGCAAAATGCTCTCTGACA	588		
565	-----GATGTGCAAAATGCTCTCTGACA	660		
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661	CTGGATCTCTGAGGACGAGCTTTAGCTTTTACTGTACCTGGTCCAGTCCCGAT	720		
649	GCTCTCAAAATCTTGGGTGTAACAAACCTGACCTGAGACCTCAGAACTTACTTTAAACCA	708		
721	GCTCTCAAAATCTTGGGTGTAACAAACCTGACCTGAGACCTCAGAACTTACTTTAAACCA	780		
709	ACAGACCTGGTTCCTGCTCTGCAATTCAGGTGTGGTCTAGAGCCAGTCTGAGAGG	768		
781	ACAGACCTGGTTCCTGCTCTGCAATTCAGGTGTGGTCTAGAGCCAGTCTGAGAGG	840		
769	GTTCGAATTCCTGCTTCCGGGAGATCCCGGTGCAACAGAGACCTCTGGCACAATAGCC	828		
841	GTTCGAATTCCTGCTTCCGGGAGATCCCGGTGCAACAGAGACCTCTGGCACAATAGCC	900		
829	AGGCTCGGGTACTCTGCCAGGGGTATGGCAGCTAGATGGCCCTGCTCTGCGGGC	888		
901	AGGCTCGGGTACTCTGCCAGGGGTATGGCAGCTAGATGGCCCTGCTCTGCGGGC	960		
889	AAGGTAACACTGTGCTGGGAGGCAACAGACAGAGTCTGCCAGCACTTGTGCCACCA	948		
961	AAGGTAACACTGTGCTGGGAGGCAACAGACAGAGTCTGCCAGCACTTGTGCCACCA	1020		

Qy	949	GTGCCCAGAAAGCACCCTGTGAATGAGCCACAAGATTTCAGTTTGGTGGAGGCTT	1080
Db	1021	GTGCCCCAGAAAGCCACTGTGAATGAGCCACAAGATTTCAGTTTGGTGGAGGCTT	1080
Qy	1009	CCCAACCTCTGTGTCCAGGTGAGCCTGTGGAGAAAGTTTCAGCTGCAAGCGTGTCTGTGG	1068
Db	1081	CCCAACCTCTGTGTCCAGGTGAGCCTGTGGAGAAAGTTTCAGCTGCAAGCGTGTCTGTGG	1140
Qy	1069	GCTCAGCTCTTTGGGGCCCTTCAAGATGATATGCTGTGTAGTGGAGATGAAAACGGGCTC	1128
Db	1141	GCTGACTCTTTGGGGCCCTTCAAGATGATATGCTGTGTAGTGGAGATGAAAACGGGCTC	1200
Qy	1129	AACAAACATCAGTCTGTGTGCTTTGGAAACCCAGTGGCTGACACCACTCCCGCAGCATGCCC	1188
Db	1201	AACAAACATCAGTCTGTGTGCTTTGGAAACCCAGTGGCTGACACCACTCCCGCAGCATGCCC	1260
Qy	1189	TCCAGGAGAGCTGCTCGCTCTGGAGAGGAGTTGTGCAAGACTTCGATCAACCAAGTGT	1248
Db	1261	TCCAGGAGAGCTGCTCGCTCTGGAGAGGAGTTGTGCAAGACTTCGATCAACCAAGTGT	1320
Qy	1249	ATGCAGCTGTGAAACGATGACAACTGGATCGCTTATGGGCTGCCCCATGACCAAGTAC	1308
Db	1321	ATGCAGCTGTGAAACGATGACAACTGGATCGCTTATGGGCTGCCCCATGACCAAGTAC	1380
Qy	1309	ATCCACAGCGCTGGGTCCCTAGTATGGCTGGCTGCTACTCTTGGCTCGGGGCTTTTC	1368
Db	1381	ATCCACAGCGCTGGGTCCCTAGTATGGCTGGCTGCTACTCTTGGCTCGGGGCTTTTC	1440
Qy	1369	TTCTTCTCTCTTAAAAAGNCCGACGAAAGCGCCGCTGGCTCCCGCACAAGCGCTTG	1428
Db	1441	TTCTTCTCTCTTAAAAAGNCCGACGAAAGCGCCGCTGGCTCCCGCACAAGCGCTTG	1500
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Qy	1489	TTGAGCCAGATGCCACTGCGGTGGCCGTGACCTGTGAGCGCCCGCAGCTGAGCGCG	1548
Db	1561	TTGAGCCAGATGCCACTGCGGTGGCCGTGACCTGTGAGCGCCCGCAGCTGAGCGCG	1620
Qy	1549	CACGGAGCCCTAGCCTGGTTCCACCAACAGCGACCGCGTATCTCTGAGGAGGTTGGGTG	1608
Db	1621	CACGGAGCCCTAGCCTGGTTCCACCAACAGCGACCGCGTATCTCTGAGGAGGTTGGGTG	1680
Qy	1609	GTAATCTCTTCTTCTGCGCCGCGCGCTGCGCAGTGTCAACAGTGGCTGAGCTCAG	1668
Db	1681	GTAATCTCTTCTTCTGCGCCGCGCGCTGCGCAGTGTCAACAGTGGCTGAGCTCAG	1740
Qy	1669	ACAGTGGAGCCCGGGCCCGCATGACCCCTCTGCGCGCTGGCTCAGCTGCTACCCGAT	1728
Db	1741	ACAGTGGAGCCCGGGCCCGCATGACCCCTCTGCGCGCTGGCTCAGCTGCTACCCGAT	1800
Qy	1729	TTCTCTGAAAGCCGGGGGACCGGCGCTACGTCGGGGTCTACTTCGACGGGTGTGTGAC	1788
Db	1801	TTCTCTGAAAGCCGGGGGACCGGCGCTACGTCGGGGTCTACTTCGACGGGTGTGTGAC	1860
Qy	1789	CCAGACTCTGTGCGCTTCCCGGTTCCGCGTGGCCCGCTCTTCTCCCTGCCACGACGCTG	1848
Db	1861	CCAGACTCTGTGCGCTTCCCGGTTCCGCGTGGCCCGCTCTTCTCCCTGCCACGCTG	1920
Qy	1849	CCGGCTTTCTGTGATGCATGCAAGGAGGCTGTCCACTTCCGCGGGGCGACCCGCGGAC	1908
Db	1921	CCGGCTTTCTGTGATGCATGCAAGGAGGCTGTCCACTTCCGCGGGGCGACCCGCGGAC	1980
Qy	1909	CGGGTGGAAACGAGTGACCCAGGCGCTGCGCTCGCCCTTGACAGCTGTACTTCTAGCTCG	1968
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Db	1201	GCNMGYTNGCNGARGARYTNTYTCARGAYTTTYMGNSNCAYCARTGYATGCARVNTGG	1260
Qy	1261	AACGATGACACATCGGATCGCTATGGCGCTGCCCATGCAAGTACTATCCACAGGCG	1320
Db	1261	AAYGATGATTAATGGGNWSYNTTGGCCTGYCCNATGGYAAATAYATHCAYMGNCN	1320
Qy	1321	TGGGTCTTAGTATGGCTGCCTGCCTACTCTGTGCTCGCGCTTTTCTCTTCCTCCTT	1380
Db	1321	TGGGTNTGTNTGGYTGTCNTGYTYTNTYNTYNGCNGCNYTNTTYTYTYTYTYNTN	1380
Qy	1381	CTAAAAAGACCGCAGGAAAGCGCGGTGGCTCCGACGCGCTTCCTCCCACTCC	1440
Db	1381	YTNAAARAGAYMGNGNAARGCNGCMGNGGNSNMGNA CNGCNYTNTYNTNCAYWSN	1440
Qy	1441	GCCGACGGAGCGGGCTACGAGCGTCTGGTGGGAGCACTGGCGTCCGGGTTGAGCGATG	1500
Db	1441	GCNGAYGGCNGCGNTAYGARMGNTYNTGNGCNGNYTNGCNGWSNCGCNYTNWSNCARATG	1500
Qy	1501	CCACTGCGCGTGGCGGTGGACCTGTGGACCGCGCGAGCTGAGCGCCACGAGGCCCTA	1560
Db	1501	CCTYTMGNTGTCNGTNGTYTNTGWSNMGMNGARYTNWSNCGNCAYGCGCNYTN	1560
Qy	1561	GCTGCTTCACACAGCAGCAGCCGCTATCTGCGAGGAGGCTGCGTGGTGAATCCTTCTC	1620
Db	1561	GCNTGCTTYCAYCAYCARMGNWGMNATHYTNCAARGAGGNGTGTWATHYTYTN	1620
Qy	1621	TTCTCGCCCGCGCGCGTGGCGAGTGTACAGCTGGCTGCAGTCCAGACAGTGGAGCCC	1680
Db	1621	TYWSNCCNGCNGTNGTCNCARTGYCARCARTGGTTNCARYTNCAACNGTNGARCN	1680
Qy	1681	GGCGCGCATGCGCCTCGCGCCTGGCTCAGCTGGGTGCTACCGATTTCTCGAAGC	1740
Db	1681	GGNCNCAYATGCTYNTGNCNGTGGTYNWSNTGYTNTNCNGAYTTYTNCARGN	1740
Qy	1741	CGGCGACCGCGCGCTAGCTGGGGTCTACTTCGACGGGCTGCTGCACCCAGACTCTGTG	1800
Db	1741	MGNCNCACNGNMGNATYGTNGGNGTNTAYTTYGAYGNYTNTNCAYCNGAYWSNGTN	1800
Qy	1801	CCCTCCCGTTCGCGTCCGCCCGCTCTTCTCCCTGCCACGAGCTGCGCGCTTTCTTG	1860
Db	1801	CCMNSNCNTYMGCTGNCNCNTNTTYMSNTYNTCCNACNCARYTNCNGCNYTYTN	1860
Qy	1861	GATGCACTGACGGAGGCTGCTCCATTCGCGGGCGCACCCGCGGACCGGCTGGGAACGA	1920
Db	1861	GAYCNYTNCARGGNGTGYWSNACNWSNCGCNGMNGCNGCNGAYVMGNTNGARMGN	1920
Qy	1921	GTGACCCAGGCGCTGCGGTCCGCGCTGGACGTACTCTAGCTCGGAAGCCCGCAGGC	1980
Db	1921	GTNACNARGCNYTNMWSNNGYNTNGAYWSNTGYACNWSNWSNWSNGRCCNCNGN	1980
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RESULT 14
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; Sequence 3, Application US/10719202
; Publication No. US20040121388A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Marine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(without alignments)
4584.824 Million cell updates/sec

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Perfect score: 2022
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113.4	55.1	2380	6	US-10-196-749-597 Sequence 597, App
2	1113.4	55.1	2380	8	US-11-311-555-13 Sequence 13, Appl
3	1113.4	55.1	2380	8	US-11-311-561-13 Sequence 13, Appl
4	1113.4	55.1	2380	8	US-11-101-316-161 Sequence 161, App
5	1113.4	55.1	2380	8	US-11-311-554-13 Sequence 13, Appl
6	1113.4	55.1	2380	9	US-11-376-673-161 Sequence 161, App
7	610.2	30.2	2350	8	US-11-293-697-1517 Sequence 1517, Ap
8	552	27.3	1864	8	US-11-293-697-313 Sequence 313, App
9	467.2	23.1	1373	8	US-11-266-748A-15241 Sequence 15241, A
10	467.2	23.1	1373	8	US-11-266-748A-64946 Sequence 64946, A
11	467.2	23.1	1373	8	US-11-266-748A-67778 Sequence 67778, A
12	444.4	22.0	757	8	US-11-266-748A-218328 Sequence 218328, A
13	444.4	22.0	757	8	US-11-266-748A-239031 Sequence 239031, A
14	406	20.1	1000	8	US-11-266-748A-293048 Sequence 293048, A
15	406	20.1	1000	8	US-11-266-748A-344477 Sequence 344477, A
16	395.6	19.6	885	8	US-11-266-748A-361313 Sequence 361313, A
17	395.6	19.6	885	8	US-11-266-748A-387553 Sequence 387553, A
18	395.6	19.6	885	8	US-11-266-748A-444692 Sequence 444692, A
19	388.8	19.2	1061	8	US-11-266-748A-361314 Sequence 361314, A
20	388.8	19.2	1061	8	US-11-266-748A-387554 Sequence 387554, A
21	388.8	19.2	1061	8	US-11-266-748A-444693 Sequence 444693, A
22	376.2	18.6	923	8	US-11-266-748A-261876 Sequence 261876, A
23	376.2	18.6	923	8	US-11-266-748A-322393 Sequence 322393, A

ALIGNMENTS

RESULT 1

US-10-196-749-597
; Sequence 597, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 597
; LENGTH: 2380
; TYPE: DNA

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Sequence 34478,
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Sequence 361315,
Sequence 387555,
Sequence 444694,
Sequence 403105,
Sequence 474151,
Sequence 6434, Ap
Sequence 62257, A
Sequence 480243,
Sequence 364072,
Sequence 447451,
Sequence 177972,
Sequence 364146,
Sequence 388228,
Sequence 447525,
Sequence 42371, A
Sequence 364147,
Sequence 388229,
Sequence 447526,
Sequence 301303,

24 359 17.8 1000 8 US-11-266-748A-293049
c 25 359 17.8 1000 8 US-11-266-748A-344478
26 313 15.5 681 8 US-11-266-748A-186516
27 312.2 15.4 1144 8 US-11-266-748A-361315
28 312.2 15.4 1144 8 US-11-266-748A-387555
c 29 312.2 15.4 1144 8 US-11-266-748A-444694
30 304.6 15.1 1000 8 US-11-266-748A-403105
c 31 304.6 15.1 1000 8 US-11-266-748A-474151
32 297.4 14.7 571 8 US-11-266-748A-6434
c 33 288.4 14.3 494 8 US-11-266-748A-62257
34 275.2 13.6 1156 8 US-11-266-748A-480243
c 35 274.4 13.6 500 8 US-11-266-748A-364072
36 274.4 13.6 500 8 US-11-266-748A-447451
37 257 12.7 939 8 US-11-266-748A-177972
38 252.2 12.5 548 8 US-11-266-748A-364146
c 39 252.2 12.5 548 8 US-11-266-748A-388228
40 252.2 12.5 548 8 US-11-266-748A-447525
41 244.4 12.1 620 8 US-11-266-748A-42371
42 235.8 11.7 810 8 US-11-266-748A-364147
43 235.8 11.7 810 8 US-11-266-748A-388229
c 44 235.8 11.7 810 8 US-11-266-748A-447526
45 58.6 2.9 941 8 US-11-266-748A-301303

D	b	1493	CTACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGSGAAGATG---ACTTGGGAAGC	1549
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Q	y	1342	TGCTACTCTTTGGCTGGCGGCTTTTCTTCTTCTCTCTTAANAAGACCGCAGGAAA	1401
D	b	1610	TGCCTACTCTTTGGCGTGGCGCTTCCCCTCATCTCTTCTCAAAAGGATCACGCGAA	1669
Q	y	1402	-----GCGGCCGTGGCTCCGCAAG	1422
D	b	1670	GGTGGCTGAGGCTTTGAACAAGACGATCCGCTCGGGGGCGGCCGCCAGGGGCGCCGCG	1729
Q	y	1423	GCTTGTGCTCTCACTCCGCGAGCGAGCGGGCTTACAGAGCTCTGGTGGGAGCACTGGCG	1482
D	b	1730	GCTCTGCTCTCTTACTTACGCCGATGACTCGGTTTCGAGCGCTGTGTGGCGGCCCTGGCG	1789
Q	y	1483	TCCGGCTTGAGCCAGATGCCACTCGCGTGGCGGTGGACCTGTGGAGCCCGCGAGCTG	1542
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Q	y	1662	-----GCTCCAGCAGTGGAGCCGGGGCGATGACGCCCTCGCGCTCGCTCAGC	1713
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Q	y	1714	TGGGTGTACCGATTTCCTGCAAGCCCGGGCGAACCGGCCCTACGTGGGGTCTATTCT	1773
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Q	y	1894	GGGCGACCCGCGGACCGGGTGGAAAGAGTGAACCAAGCGCTCGGTTCGCCCTCGACAGC	1953
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RESULT 3
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, Sequence 13, Application US/11311561
, Publication No. US2006008917A1
, GENERAL INFORMATION:
, APPLICANT: Genentech, Inc.
, APPLICANT: Chen, Jian
, APPLICANT: Filvaroff, Ellen
, APPLICANT: Fong, Sherman
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul
, APPLICANT: Grimaldi, Christopher
, APPLICANT: Gurney, Austin
, APPLICANT: Li, Hanzhong
, APPLICANT: Hillan, Kenneth
, APPLICANT: Tumas, Daniel
, APPLICANT: Vanloocker, Menno
, APPLICANT: Vandelen, Richard
,

```

; APPLICANT: Watanabe, Colin
 ; APPLICANT: Williams, P.Mickey
 ; APPLICANT: Wood, William
 ; APPLICANT: Yansura, Daniel
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C1P1(US)
 ; CURRENT APPLICATION NUMBER: US/11/311,561
 ; CURRENT FILING DATE: 2005-12-20
 ; PRIOR APPLICATION NUMBER: US/09/747,259
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/172,096
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/31274
 ; PRIOR FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: US 60/175,481
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 60/191,007
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/07532
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 39
 ; SEQ ID NO 13
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-11-311-561-13

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QY	61	CTGGAGACACTGATGGAGCCTCAGGACACTGCACGCTGCTCTTAGGCCCTCTCTGCGCAC	120		
Db	293	CTGGAGAGGCTTGTGGGCGCTCAGGACCGTACCCACTGCTCTCGGCGCCTCTCTCTGCGCGC	352		
QY	121	CTCTGGGATGTGACGTGCTCTGCTGCTGGAAACCTCCAGTCTGCGCCCGACGGCCCTGTG	180		
Db	353	CTCTGGGACAGTGACATACTCTGCTGCTGGGACATCGTGCTGCTCTCGGCGCCCGCTG	412		
QY	181	CTAGTGCCATACCGCCTGCACAGCGAGCTGCTGAGGTCTCCACAGAAACAGATGTC	240		
Db	413	CTGGCGCCTACGCACTCTGCACAGAGCTGCTGTGAGTGTGCCAGAGGAGACCGACTGT	472		
QY	241	GCCCTTCCTGTCCGTGTGGTGTGCTTCCACTTGGCCGTFGCATGGGCACTGGGCGAGCCTGAA	300		
Db	473	GACCTCTGCTGCTGTGGCTGTCCACTTGGCCGTFGCATGGGCACTGGGCGAGCCTGAA	532		
QY	301	GAAGCTGGAAAGT-----CTGATTTCAGAACTCCAGGAGCTTAGGAAACGCTCT	348		
Db	533	GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGAGCCTTAGGNAAGCTCT	592		
QY	349	CTTCAGGCCCGAGTGGTGTCTCTCTCCAGGCGCTACCCCATCGCCCGCTGTGCGCCTGTG	408		
Db	593	CTTCAGGCCCGAAGTCTGTCTCTCTTCAGGCGCTACCCCTACTGCGCCGCTGCGTCTCTGTG	652		
QY	409	GAGGTCCAGGTGCGCGCTGACTGTGTFGACGCTGTGTCAGTCCGTGGGTCTCGGGTATTT	468		
Db	653	GAGGTGCAAGTCCCTGCTGCCCTTGTGTCAGTTTGGTTCAGTCTGTGGGCTCTGTGGTATAT	712		
QY	469	GACTGTTTCGAGGCTAGTCTTGGGGCTGAGGTACAGATCTGCTCTCTACAGGAAGCCACAG	528		

			713	GACTGCTTCGAGGTGCCCTAGGAGTGAAGTACGAATCTGGTCTTATCTCAGGCCCGG	712
	QY	TACCAGAAAGAGCTCAACCTCACACAGCAGCTGCCT	529	TACCAGAAAGAGCTCAACCTCACACAGCAGCTGCCT	564
	DB	773 TACGAGAAGGAACCTCAACCAACAACAGCAGCTGCTGCCCTGCCCTCAACGTGTCA	832		
	QY	565 --- GATGGTGACAAATGCTCTTTCCACACTGGANGTCTCTGAGGAGCAGGACTTTAGCTTC	621		
	DB	833 GCAGATGGTGACAAACGTGCACTCTGGTTCTGAAATGCTCTGAGGAGCAGCACTCGGCCTC	892		
	QY	622 TTACTGTACTCGCTCCAGTCCCAGTAGCTCTCAAATCCCTTGTGGTACAAAACCTCACT	681		
	DB	893 TCCCTGTACTGGAATCAGGTCAGGGCCCCCAAAACCCCGGTGGCACAAAAACCTCACT	952		
	QY	682 GGACTCTAGAACATTACTTTAAAAACAACAGACCTGGTTCCCTGCCCTCTGCAATTCAGGTG	741		
	DB	953 GGAACGACATCATTA CTTTGAACCAACAGACCTGGTTCCCTGCCCTCTGTATTCAGGTG	1012		
	QY	742 TGTCGCTAGACGACAGCTCTGAGAGGGTCAAAATCTGCCCTTCGCGGAAGATPCCCGT	801		
	DB	1013 TGGCTCTTGGAACTCTGCTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACCCCGC	1072		
	QY	802 GCACACAGGACCTCTGGCAATAGCCAGCTGCGGGTACTGTCTCCACAGGGGTATGCGAG	861		
	DB	1073 GCACACAGAACCTCTGGCAAGCCGCCGACTGCGCACTGTCTGCAACCTTCACAGAGCTGGCTG	1132		
	QY	862 CTAGATCGCTTGCCTGTCTGSCGGGCAAGGTAACTGTCTGTGGCAGGACACAGACCAAG	921		
	DB	1133 CTGACACGACCGTGTCTGCTGCCCGCAGAGCGGCACTGTCTGCGCGGCTTCGCGTGGG	1192		
	QY	922 AGTCCCTGCCACGCACTTTGTGCCACCACTGCTGCCAGGAAGAACGCACTGTGAAATGAGCCA	981		
	DB	1193 GACCCCTGCCAGCCACTGCTCCCAACCGCTTTCTGGGAGAAAGTCACTGTGGACAAGGTT	1252		
	QY	982 CAAGATTTCCAGTTGGTGCGAGGCCACCCCAACCTCTGTGTCTCAGGTTGAGCACTGCGAG	1041		
	DB	1253 CTCGAGTTTCCCAATTCGTGAAGGCCACCCCTAAACCTCTGTGTTCAGGTTGAACAGCTCGAG	1312		
	QY	1042 AAGGTTTCAGCTGCAAGCGTGTCTGTGGGCTGACCTCTTTGGGGCCCTTCAAGGATGATATG	1101		
	DB	1313 AAGCTGAGCTTGACAGGAGTGTCTGTGGCTGACTCTCTGGGCGCTCTCAAGACGATGTG	1372		
	QY	1102 CTGTTAGTGGAGATGA AAAACCGGCTCAACAACAATCATGCTGTGCTTTGGAAACCCAGT	1161		
	DB	1373 CTACTGTTGGAGACA CGAGGCCCCACGAGCAACAGATCCCTCTGTGCTTTGGAACCCAGT	1432		
	QY	1162 GGCTGTATAACA CTGCCAGCATGGCTTCAACGAGAGCTGTCTGCCCTGGGAGAGAGTTG	1221		
	DB	1433 GGCTGTACTTCACTACCCAGCAAAAGCTTCCACGAGGGCAGCTCGCTTGGAGAGTACTTA	1492		
	QY	1222 CTGCAAGACTTCCGATCACACCATGTGTATGCAGCTGTGGAACGATGACATATGGGATCG	1281		
	DB	1493 CTAACAAGCTTGCACTGAGCCAGTGTCTGACGTATGGAACGATG--- ACTTTGGAGCG	1549		
	QY	1282 CTATGGGCTGCCCCATGGAACAATATCAACAGGGCTGGGTCTCTAGTATGGCTGGCC	1341		
	DB	1550 CTATGGGCTGCCCCATGGAACAATA CATCCACAAGCGCTGGGCCCTCGTGTGCTGGCC	1609		
	QY	1342 TGCTACTCTTGGCTGCGGCGTTTTTCTTCTCTCTTCTA AAAGAGACCGCAGAGAA	1401		
	DB	1610 TGCTACTCTTTGGCGCTGCGCTTTTCCCTCATCTCTCTTCTCAAAAAGGATCAGCGCAAA	1669		
	QY	1402 -----GGGGCCCGTGTCTCCCGCAAG	1422		
	DB	1670 GGTGGGTGAGGCTCTTGAAACAAGACGTCGCTCGGGGGCGCGCCGCAAGGGCGCGCG	1729		
	QY	1423 GCCTTGTCTCTTCACTCGCGCGAGCGGGCTTACGAGCGCTCTGTGTGGAGCAGCTGCGC	1482		
	DB	1730 GCTCTGTCTCTTACTCAGCCGATGACTCGGGTTTCAGCGCCTTGTGTGGCGCCTGCGC	1789		
	QY	1483 TCOCGTTTGAGCCAGATGCCACTCGCGGTGGCGCTGTGACCTGTGTGAGCCGCGCGAGCTG	1542		

Db	1790	TCGGCCCTGTGCGAGCTGCGCGCTGCGCGTGGCGGTAGACTGTGTGGAGCCGTCGTGAAC	1849
Qy	1543	AGCGCGCACGGAGCCCTAGCCTGTGTTCCACCAACAGCGAGCCGCGTATCTCTGCAGGAGGGT	1602
Db	1850	AGCGCGCAGGGGCCGTGGCTTGGTTTTCAGCGCGCAGCGGGCCAGACCCCTGTCAGGAGGGC	1909
Qy	1603	GGCGTGGTAATCTTCTCTCTCCCGCGGGCCGTTGGCGCAGTGTGAGCAGTGGCTGCA -	1661
Db	1910	GGCGTGGTGTCTTGTCTTCTCTCCCGTGGCGGTGGCGTGTGTGTGTGTGTGTGTGTGTGTGT	1969
Qy	1662	-----GCTCCAGACAGTGTGAGCCCGGGCCGACATGACGCCCTCGCGCCTGGCTCAGC	1713
Db	1970	GATGGGGTGTCCGCGGCCGCGGGCGCAGCGCCCGCACGACGCGCTTCCGCGCTCGCTCAGC	2029
Qy	1714	TGCGTGTCTACCAATTTCTGTGAAGCGCGGGCGACCGGGCGCTACGTTCGGGGTCTACTTC	1773
Db	2030	TGCGTGTCTCCCGACATTTCTTGTGAGGGCCGGGCGCCCGCGACGTACGTGGGGGGCTTGTCTC	2089
Qy	1774	GAGGGGTGTGTGACCCAGACTCTGTGTCCCTCCCGCTTCGCGCTCGGCCCGCTCTTCTCC	1833
Db	2090	GACAGGCTGTCTCACCGGAAGCGGTACCGGCCCTTTTCGACACCGTGC CGCTTTCACA	2149
Qy	1834	CTCGCCACGACGTGCGGGTTTCTGTGATGTCACTGTGAGGAGGCTGTCTCCACTTTCGGCG	1893
Db	2150	CTCGCCCTCCCACTGCGCAGACTTCTCTGGGGGCCCTGTGACGAGCTCTGCGGCCCGCGTTC	2209
Qy	1894	GGCGACCCCGGACCGGGTGGAAAGAGTGTACCCAGCGCGTGTGGGTTCGGCCCTGTGGAC	1953
Db	2210	GGCGGGTCCAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTTCAGCCAGCCCTGGATAGC	2269
Qy	1954	T-GTACTTCTAGCTGTGGAAGCCCGACGGCTGTCTGTGAGGAATGGACCTGGGAC	2005
Db	2270	TACTTTCATCCCGGGGACTCCCGCGCCGGGACGCGGGGTGTGGACACAGGGGC	2322

RESULT 4

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US-11-101-316-161
; Sequence 161, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P2230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 161
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-161

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Query Match	55.1%	Score 1113.4;	DB 8;	Length 2380;
Best Local Similarity	73.6%	Pred. No. 3.2e-265;		
Matches 1541;	Conservative	0;	Mismatches 461;	Indels 91;

1118	Db	GCCTCGTGTGCTGGCGTGCCTACTCTTTCGCGCTGGCTTCCCTCATGCTCTCTTC	1177
1384	Qy	AAAAAGGACCGCAGAAAGCGGCCGTGGCTCCCGCAGCGGCTTGTCTCTCCACTCCGCC	1443
1178	Db	AAAAAGGATACGCGAAAGCGGCCGAGGGGCCGCGGCTCTGCTCTCTACTACAGCC	1237
1444	Qy	GACGGAGGGGCTACGAGCGTCTGGTGGGAGCACTGGGGTTCGGGTTGAGCCAGATGCCA	1503
1328	Db	GATGACTCGGGTTTCGAGCGGCTCTGGTGGGCGCCCTGCGCTCGGCCCTGTGCCAGCTCCG	1297
1504	Qy	CTGCGCTGGCGCTGGGACCTGTGAGAGCCGCCCGCAGCTGAGCGCGCACGAGACCCCTAGCC	1563
1298	Db	CTGCGCTGGCGGTAGACCTGTGAGCGCGTCTGTAACCTGAGCGCGCAGGGGCCGTGGCT	1357
1564	Qy	TGTTTCACACACAGCAGCGCGCTATCTGTGAGAGGGTGGCTGTGTAACTTCTCTTC	1623
1358	Db	TGTTTTCACGCGCAGCGCGCGCAGACCTCTGAGAGGGCGCGTGTGTGTCTTCTTTC	1417
1624	Qy	TCGCCCCGGCGTGGCGCAGTGTTCAGCAGTGGCTGCA-----GCTCCAGACAGTG	1674
1418	Db	TCTCCCGTGGGTGGCGCTGTGACGAGTGGCTACAGATGGGTGTTCGGGCCCGG	1477
1675	Qy	GAGCCCGGGCGCATGACGCCCTCGCGCTGGCTCAGCTTCGCTGTACCCGATTTCTCTG	1734
1478	Db	GCGCACGGCCCGCACGACGCGCTTCGCGGCCCTCGCTCAGCTTCGCTGTCCCGCATTCTTG	1537
1735	Qy	CAAGCCGGGGGACCGCGCGCTAGCTCGGGTCTACTTTCGACGGGCTGTGCAACCCAGAC	1794
1538	Db	CAGGGCCGGGGCGCCCGGACGTACGTGGGGGCTGTCTTCGACAGGCTGTCTCCACCCGGAC	1597
1795	Qy	TCTGTGCCCTCCCGCTTCGCGCTCGCCCCGCTCTTCTCCCTGCCCCAGCAGCTGCCGGCT	1854
1598	Db	GCGGTACCCGCCCCCTTTTCGCACGGTGCCCCGTCTTCACTATGCCCTCCCACTGCCAGAC	1657
1855	Qy	TTCTGTGATGCATGTGAGGAGGCTGTCTCACTTTCGCGGGGGGAGACCCGCGGACCGGGTG	1914
1658	Db	TTCTTGGGGGCCCTTGCAAGCAGCCTTCGCGCCCCCGCTTCGCGGGCGGCTCCAGAGAGAGCG	1717
1915	Qy	GAACGAGTGACCCAGGCGCTGCGTCCGCTCGACAGCT-GTACTTCTAGCTCGGAAGC	1973
1718	Db	GAGCAGTGTCCCGGGCCCTTCAGCAGACCTCTGATAGCTACTTCCATCCCCCGGGACT	1777
1974	Qy	CCCAGGCTGTGGAGGAATGGGACCTGGGAC	2005
1778	Db	CCCGCGCCGGGACGCGGGGTGGACACGAGGGCG	1809

RESULT 9

RESOL 3
US-11-266-748A-15241/c
; Sequence 15241, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276

[illegible]

/	PRIOR APPLICATION NUMBER:	EP 04105483.4			
/	PRIOR FILING DATE:	2004-11-03			
/	PRIOR APPLICATION NUMBER:	EP 04105507.0			
/	PRIOR FILING DATE:	2004-11-03			
/	PRIOR APPLICATION NUMBER:	EP 04105485.9			
/	PRIOR FILING DATE:	2004-11-03			
/	PRIOR APPLICATION NUMBER:	EP 04105484.2			
/	PRIOR FILING DATE:	2004-11-03			
/	PRIOR APPLICATION NUMBER:	US 60/662,276			
/	PRIOR FILING DATE:	2005-03-14			
/	PRIOR APPLICATION NUMBER:	US 60/700,293			
/	PRIOR FILING DATE:	2005-07-18			
/	NUMBER OF SEQ ID NOS:	483996			
/	SOFTWARE:	PatentIn version 3.3			
/	SEQ ID NO	239031			
/	LENGTH:	757			
/	TYPE:	DNA			
/	ORGANISM:	Homo Sapiens			
/	US-11-266-748A-	239031			
Query Match 22.0%; Score 444.4; DB 8; Length 757;					
Best Local Similarity 76.7%; Pred. No. 5e-100;					
Matches 557; Conservative 0; Mismatches 166; Indels 3; Gaps 1					
Qy	679	ACTGGACCTCAGAACATTACTTTAAACCACACAGACCTGTGTTCCCTGCCTTCGCAATTCAG	738		
Db	1	ACTGGACCGCAGATCATTTACTTGAACCACACAGACCTGTGTTCCCTGCCTTCGTATTTCAG	60		
Qy	739	GTTGTGTCGTCTAGAGCCAGACTCTGAGAGGGTGGAATTCGCCCTTCGGGAGAGATCCC	798		
Db	61	GTTGTGCCCTCTGGAACTCTGACTCGTTAGGAGGAACATCTGCCCTTCAGGGAGGACCCC	120		
Qy	799	GGTGCAACAGAAACCTCTGGCACATAGCACCGCTCGGGGTACTGTTCCTCCAGGGGTATGG	858		
Db	121	CGGCACACAGAACTCTGGCAGCCGCCCCACTGCGACTGCTGACCTTCGACCTTCGAGAGCTGG	180		
Qy	859	CAGCTAGATGCGCTTGTCTGTCTGCGCGCAGAGGTAAACAATGTCGTGCGCAGGACACAGAC	918		
Db	181	CTGCTGGAGCGACCTGTGCTCGTCCCGCAGAGCGGCACCTGTGCTGCGGGCTCCGGGT	240		
Qy	919	CAGAGTCCCTGCGACGCCACTTGTGTGCACAGTGCCTCCAGAGAAGCACCCTGTGTAATGAG	978		
Db	241	GGGGACCCCTGCACGCCACTGTGTCCA CCGCTTTCCTGGGAGAAGCTCCTGTGGACAAG	300		
Qy	979	CCACAAGATTTCAGTTGGTGGCAGGCCACCCCAACTCTGTGTCCAAGGTGAGCACCTGG	1038		
Db	301	GTTCTCGAGTTTCCCATTTGCTCAAAGGCCACCCTAACTCTGTGTTCAGGTGAACAGCTCG	360		
Qy	1039	GAGAAGGTTTCAGCTGCAAGCGTCTGTGGGTGCACTCTCTGGGGCCCTTCAAAGTAGAT	1098		
Db	361	GAGAAGCTGCAGCTGCAGBAGTGTCTGTGGGTGACTCTCCCTGGGGCTCTCAAGACGAT	420		
Qy	1099	ATGCTGTTAGTGGAGATGMAAACCGGCTCAACAACACATCACTGTGCTTGGAACTCC	1158		
Db	421	GTGCTACTGTTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCTTGGAACTCC	480		
Qy	1159	AGTGGCTGTACCACTGCCAGCATGGCCCTCCACGAGAGCTGCTGCGCTGGGAGAGGAG	1218		
Db	481	AGTGGCTGTACTTCACTACCCAGCAANGCCTCCAGAGGGCAGCTGCGCTTGGAGAGTAC	540		
Qy	1219	TTCCTGCAGACATTTCCGATCACACCAAGTGTGACGCTGTGGAAACGATCAACAATGGGA	1278		
Db	541	TTACTACAAGACCTTCAGTCAGGCCAGTGTCTGACCTATGGACGATG---ACTTGGGA	597		
Qy	1279	TCGCTATGGGCTTCCCCCATGGACAAGTACATCCACAGCGCTGGGTCTCTAGTATGGCTG	1338		
Db	598	CGGCTATGGGCCCTGCCCCCATGGACAAATACATCCAAGCGCTGGGCCCTCTGTGTGGCTG	657		
Qy	1339	GCCTGCTACTCTTGGCTGGCGGCTTTCTTCTTCCTCTCTAAAAAGGACCGCAGG	1398		
Db	658	GCCTGCTACTCTTTTGCCGCTGGGCTTTCCCTCATCTCTCTCAAAAAGGATCACGCG	717		
Qy	1399	AAGCG 1404			

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Db          |||||
            718 AAACGG 723

RESULT 14
US-11-266-748A-293048
; Sequence 293048, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 293048
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-293048

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[illegible]

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QY 1558 CTAGCTGGTTCCACCACGACGCGCTATCTCTGAGGAGGTGGCTGGTAATCTT 1617
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Db 418 GTGGCTGGTTTTCAGCGGACGCGGCCAGACCTCTGACGAGGGGCGGTGGTCTTG 477
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1618 CTCTTCTCGCCCGGGCGGTGGCGAGTGTACAGAGGTGTGAGCT-----CCAG 1668
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 478 CTCTTCTCTCCCGTGGGTGGCGCTGTGACGAGTGGCTACAGGATGGGGTGTCCGGG 537
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1669 ACAGTGGAGCCCGGGCGCATGACGCTCGCGCCCTGGCTCAGCTCGCTACCCGAT 1728
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 538 CCGGGGCGCACCGCGCCGACGAGCTTCCGGCCCTCGCTCAGCTCGCTGCTGCCGAC 597
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1729 TTCTCTCAAGCCCGGGGACCGGCGCTAGCTCGGGGTCTACTTCGACGGGCTGCTGCAC 1788
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 598 TTCTTGCAGGGCCGGGCGCCGAGAGTACTGTGGGGCTTGTTCGACAGGCTGTCTCCAC 657
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1789 CCAGACTGTGTGCTTCCCGTTCGCGTCCGCGTCCGCTTCTTCTCCCTGCCCCACGCACTG 1848
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 658 CCGGACGCGGTACCGCGCTTTTCCGACCGTGCCTTTCACACTGCGCTCCCAACTG 717
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1849 CCGGCTTCTCTGATGCATGACGAGGAGGTGCTTCACTTCCGCGGGGACCCGCGGAC 1908
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 718 CCAGACTTCTTGGGGGCTTGCAGAGCTTCGCGCCCGCTTCCGGGGGCTCCAAAGAG 777
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QY 1909 CCGGTGGAACTGACCCAGCGGCTGCGGTCCGCTCGCTGACAGCT-GTACTTCTAGCTC 1967
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Db 778 AGAGCGGAGCAAGTGTCCCGGCTTTCAGCAGCCCTGTGATAGCTACTTCCATCCCCCG 837
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1968 GGAAGCCCCAGGCTGTGCGAGAAATGGGACCTGGGAC 2005
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 838 GGGACTCCCGCGCGGACGCGGGGTGGGACGAGGGGC 875
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RESULT 15

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US-11-266-748A-344477/c
; Sequence 344477, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIORITY FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 344477
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-344477
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Query Match 20.1%; Score 406; DB 8; Length 1000;
Best Local Similarity 70.7%; Pred. No. 1.8e-90;
Matches 621; Conservative 0; Mismatches 205; Indels 52; Gaps 4;
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QY 1177 CCAGCATGCGCTCCACGAGAGCTGCTCGCTGGGAGAGAGTGTGCTCAAGACTTCCGA 1236
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1000 CCAGCAAAAGCTCCACGAGGGCAGCTCGCTTGGAGAGTACTTACTACAAAGACTGGAG 941
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1237 TCACACAGTGTATGACAGCTGTGGAACGATGACAAATGGGATCGCTATGGGCTGCCCC 1296
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 940 TCAGGCCAGTGTCTGACAGCTATGGACGATG---ACTTGGAGAGCTATGGGCTGCCCC 884
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1297 ATGGAAGAATACATTCACAGCGCTGTAGTATGTAGTATGGCTGCGCTACTCTTGGCT 1356
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Db 883 ATGGACAAAATACATTCACAAAGCGTGGGCTCTGTGTGGTGGCTGCTACTCTTTGCC 824
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QY 1357 GCGGCGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1401
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 823 GCTGCGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 764
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QY 1402 -----GCGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1437
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Db 763 TTGAAACAGAGCTGCTCGCTCGGGGGCGGCGCCAGAGGGGCGCGGCTCTGCTCTCTAC 704
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QY 1498 ATGCCACTGCGCTGCGCTGGGAGCTGTGTGAGCGCGCGAGCTGAGCGGACGAGGCC 1557
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Search completed: August 17, 2006, 00:44:15
Job time : 720 secs

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 20:59:40 ; Search time 11525 Seconds

(without alignments)

11219.235 Million cell updates/sec

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Perfect score: 2022

Sequence: "1 atgcctgtcctcgttcct.....gacctgcactacactagaa 2022

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_env.*

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6: gb_ro.*

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8: gb_ev.*

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10: gb_vi.*

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14: gb_on.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2022	100.0	2256	2	AX360307	Sequence
3	1980.2	97.9	2269	2	CS251263	Sequence
4	1962.2	97.0	2287	2	CS251267	Sequence
5	1940	95.9	2328	2	AX360310	Sequence
6	1933.6	95.6	2314	2	CS135270	Sequence
7	1933.6	95.6	2314	2	AX350976	Sequence
8	1929.6	95.4	2331	2	AX720728	Sequence
9	1412.2	69.8	2022	2	AX360309	Sequence
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11	1330.2	65.8	2094	2	AX360312	Sequence
12	1327.6	65.7	2094	2	AX350978	Sequence
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14	1162.4	57.5	2255	2	AX073993	Sequence
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16	1113.4	55.1	2380	2	CS257646	Sequence
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28	1069.2	52.9	2180	2	CS251261	Sequence
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43	960.8	47.5	2314	2	AX720676	Sequence
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ALIGNMENTS

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DEFINITION	AF458066				
ACCESSION	AF458066.1	GI:21779859			
VERSION					
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 2153)				
AUTHORS	Gilbert, J.M. and Gorman, D.M.				
TITLE	Identification of novel IL-17 related receptors				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2153)				
AUTHORS	Gilbert, J.M. and Gorman, D.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-DEC-2001) Genomics, DNAX Research Inc., 901 California Ave., Palo Alto, CA 94304, USA				
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Qy	121	CTCTGGGATGGTGACGTGCTCTGCTCGCTGGAGCCTCCAGTCTGCCCGCAGGCCCTGTG	180			
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Qy	181	CTAGTGCTTACCCGCTCGACACGGAGCTGGTGTCTGAGGTGTCCACAGAAAGACAGATTGC	240			
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Qy	481	GCTAGTCTTTGGGGCTGAGGTACAGATCTGTGCTTACAGAACCCAGTACCAGAAAGAG	540			
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Qy	901	TGCTGGCAGGCCACAGACCTAGAGTCCCTGCCAGCCACTTGTGCCACAGTGTGCCAGAG	960			
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DEFINITION	Sequence 25 from Patent WO2005123778.		
ACCESSION	CS251263		
VERSION	CS251263.1	GI:85361024	
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Mus musculus		
REFERENCE	1 Presnell, S.R.		
AUTHORS	Soluble zcytor14, anti-zcytor14 antibodies and binding partners and		
TITLE	methods of using in inflammation		
JOURNAL	Patent: WO 2005123778-A 25 29-DEC-2005;		
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Qy	61	CTGAGAGACATGATGAGACCTCAGGACATGTCAGCGTCTCTTAGGCGCTCTCTTGGCCAC	120
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ACCESSION CS251267
VERSION CS251267.1 GI:85361025
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ORGANISM Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1

AUTHORS Presnell, S.R.
TITLE Soluble zcytor14, anti-zcytor14 antibodies and binding partners and methods of using in inflammation
JOURNAL Patent: WO 2005123778-A 29 29-DEC-2005;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
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Matches 2019; Conservative 0; Mismatches 3; Indels 45; Gaps 1;
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RESULT 6

CS135270
LOCUS
Sequence 7 from Patent WO2005065711.
2314 bp DNA linear PAT 09-AUG-2005

DEFINITION

CS135270

ACCESSION

CS135270

VERSION

CS135270.1 GI:72067721

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

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Gorman, D.M.

Mammalian receptor proteins; related reagents and methods

Patent: WO 2005065711-A 7 21-JUL-2005;

Schering Corporation (US)

Location/Qualifiers

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REFERENCE	Haudenschild, D., Rose, L., Moseley, T. and Reddi, A. H.
AUTHORS	IL-17 receptor-like protein, uses thereof, and modulation of
TITLE	catabolic activity of il-17 cytokines on bone and cartilage
JOURNAL	Patent: WO 0238764-A 74 16-MAY-2002;
	The Regents of the University of California (US)
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ACCESSION	AX720728				
VERSION	AX720728.1	GI:29892514			
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RESULT 9
AX360309
LOCUS AX360309 2022 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO0204519.
ACCESSION AX360309
VERSION AX360309.1 GI:18675811
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Gao, Z.
TITLE Murine cytokine receptor
JOURNAL Patent: WO 0204519-A 3 17-JAN-2002;
ZymoGenetics, Inc. (US)
LOCATION/Qualifiers
FEATURES
source
1..2022
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/note="This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2."

ORIGIN
Query Match 69.8%; Score 1412.2; DB 2; Length 2022;
Best Local Similarity 56.2%; Pred. No. 0;
Matches 1137; Conservative 464; Mismatches 421; Indels 0; Gaps 0;

Qy 1 ATGCCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 ATGCCGTGWSNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy .61 CTGGAGAGACTGATGGAGCCTCAGGACACTGACGCTGCTCTAGGCTCTCTCTGCTGCTGCT 120
Db 61 YTNAGRMGNNTNATGGARCCNCARGAYACNGCNMNTGYWSNYTNGNYTNWSNTGYCAY 120
Qy 121 CTCCTGGATGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 YTNCTGGAGYGNNGAYGTYNTGTYTNCNGNWSNYTNCARWSNGCNCCNGNCCNGTN 180
Qy 181 CTAGTGCCTTACCCGCTGCAGACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 YTNCTGNCNACNMGNNTNACARACNGAR YTNCTGTYTNGNTGYCCNCAARACNGAYTGY 240
Qy 241 GCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 GCNYTMNGNMTNMNGTNGTNGTNCAYTNGCNGTNCAYGNGNCA YTGCGNCAACNGAR 300
Qy 301 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAACGCTCTCTCCAGGCCAC 360
Db 301 GARGCNGGNAARWSNGAYWSNGAR YTNCAARGARWSNMGNAA YGNCNWSYTNCAARGCNCAR 360
Qy 361 GTGTGCTCTCTCTCCAGGCTTACCCCATCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 GTNGTNTWSNTTYCARGCNTAYCCNATHGCMGNTGYCNYTNYTNGRTNARGTNCARGTN 420
Qy 421 CCCGCTGACCTGGTGCAAGCTGGTTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 CCNGCNGAYTNGTNCARCCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 480

QY	481	GCTAGTCTTGGGCTGAGGTACAGATCTGGTCTCTACACGAGCCAGGTCACGAAAGAG	540
Db	481	GCWNSYNTGNGGNGARGTNCARATHTGWSNTAVACNAARCCNMGNNTAYCARAARGAR	540
QY	541	CTCAACCTCACACAGAGCTGCCGTGATGAGTGAACATGCTCTTGACACTGGATGCTCT	600
Db	541	YTNAAAYTNACNARCARYTNCNGAYGGNGAYAAAYGTNTYNTNACNYNGAYGTNWSN	600
QY	601	GAGCAGAGGACTTTAGCTTCTTACTGTACTGTCTGCTCCAGTCCCGGATGCTCTCAATCC	660
Db	601	GARGCARGAYTTYSNTYNTYNTAYTNMGNCNGTNCNGAYGNYTNAARWSN	660
QY	661	TTTGTTGTAACAAAACCTGACCTGACACCTCAGAACATTACTTTAAACACACAGACCTGGTT	720
Db	661	YNTGGTAYAAARAAAYTNACNNGNCCNCAARAAYATHACNYTNAAYCAYACNGAYTNGTN	720
QY	721	CCCTGCTCTCANTTCAGTGTGGTCCGTAGACGCACTCTGAGAGGGTCSAAATTCCTG	780
Db	721	CNTGYTNTGTATHCARTWTGWSNTYNGARCCNGAYNSGARMGNGTNGARTTYTG	780
QY	781	CCCTTCCGGGAAGATCCCGGTGCACACAGGAACCTCTGGCACATAGCACGCTCGGGTA	840
Db	781	CCNTTYMGNGARGAYCNGGNGCNCAYMGNAAYYTNTGGCAYATHGCMNGYTNMGNTN	840
QY	841	CTGTCCCAAGGGTATGCAGCTAGATCGCTCTGCTGCGGGCAAGTAACTG	900
Db	841	YTNWSNCCNGGNTTGGCARTYNGAYGNCNTGYTGYYTNCNGNAAAGRTNACNYTN	900
QY	901	TGCTGCGAGCCACACAGAGTCCCTGCCAGCACCTTGTGCCACACAGTCCCCAGAG	960
Db	901	TGTTGGCARGCNCNGAYCARWSNCCNTGYCARCCNYTNGTNCNCCNGTNCNCARAR	960
QY	961	AACGCCACTGTGAATGAGCCACAAGATTCCAGTTGTGGCAGGCCACCCCAACCTCTGT	1020
Db	961	AAYGCCNACNGTNAAYGARCNCARGAYTTYCARYTNGTNGCNGNCAYCCNAAYYTNG	1020
QY	1021	GTCCAGGTGAGCACCTGGGAGAAGTTTACGTGCGAAGCGTGTCTGTGGGTGACTCCCTTG	1080
Db	1021	GTNCARGTWNACNTGGARAARGTNCARYTNCARGCNTGYWSNTGGGNGAYWSNTN	1080
QY	1081	GGGCCCTTCAAGATGATGTGTTAGTGGAGATGAARACCGGCTCAACAACACATCA	1140
Db	1081	GGNCNTTAAARGAYGATGYTNTYNTGNGARATGAARACNGYNTNAAAYACNWSN	1140
QY	1141	GTCTGTGCTTGAACCACTGCTGTACACCACTGCCAGCATGCCCTCCACGAGACT	1200
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QY	1201	GCTCGCTGGGAGGAGTGTGCAAGACTTCGATCACACAGGTATGACGCTGTGG	1260
Db	1201	GCNMGNTNGNGARGARYTNTNCARGAYTTYMGNWSNCAYCARTGYATGCARYTNTGG	1260
QY	1261	AACGATCACACATGGGATCGCTATGGCTGCGCCATGACCAAGTACATCCACAGCGC	1320
Db	1261	AAYGAYGAYAAATGGGWSNNTYNTGGCNTGYCCNATGAYAAATAYATHCAYMGNMG	1320
QY	1321	TGGTCTCTAGTATGGCTGCTACTCTGTGCTCGCGGCTTCTCTCTCTCTCT	1380
Db	1321	TGGTNTYNTGTYTNGTNGTNTYNTYNTYNTGNCNGCNYTNTTYTYTYTYTYTYTN	1380
QY	1381	CTAAAAAGGACCCGAGAACCGCGCTGGCTCCCGCAGCGCTTGTCTCTCCACTCC	1440
Db	1381	YTNARAARGAYMGNMGNAACGNCNGNNGNWSNMGNCNCGNYTNTYNTNCAYSN	1440
QY	1441	GCCAGCAGGCGGGCTACGAGCGTCTGTGGAGACATGGCGTCCGGTTCAGCCAGATG	1500
Db	1441	GCNGAYGGCNGGNTAYGARMGNTYNTGNGCNGTNGCNGWSNCGNYTNWSNCARATG	1500
QY	1501	CCACTGCGCTGGCGCTGACCTGTGGAGCCGCGAGCTGAGCGGACGAGCCCTA	1560
Db	1501	CCNYTMNGTNGCNGTNGAYTNTTGGWSNMGNGARGARYTNWSNCGNCAYGGGNCYTN	1560
QY	1561	GCCTGTTTCCACCAACGAGCGCGGTATCTCTCAGAGGGTGGCGTGAATCTTCTC	1620
Db	1561	GCNTGGTTYCAYCAYCARMGNGMNGNATHYTNARGARGNGNGTNGTNGTNTYNTN	1620
QY	1621	TTCTCGCCCGCGCGGTGGCGCAGTGTCCAGCAGTGGGTGCGAGCTCCAGACAGTGGAGCC	1680
Db	1621	TTYWSNCCNCGNCGTNGCNCARTGYCARCTGGYTNCARYTNCARACNGTNGARCCN	1680
QY	1681	GGCCCGCATGACGCCCTCCCGCTGGCTAGCTGCTGCTACCCGATTTCTCTCAAGGC	1740
Db	1681	GGNCNCNAYGAYGNYTNGCNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG	1740
QY	1741	CGGCGCACCGCGCTAGCTGGGGTCTACTTCGACGGGCTGCTGCACCCAGACTCTGTG	1800
Db	1741	MGNGNACNMGNMNTAYTNGNGTNTAYTYTGAYGNYTNTNCAYYCNGAYWSNGTN	1800
QY	1801	CCCTCCCGCTTCCCGGTGCGCCCTCTCTCTCTGCCCCACGACCTGCCGCTTCTCTG	1860
Db	1801	CCNWSNCCNTTYMNGTNGCNCNTYTNWSNTNCCNACNARYTNCNCGCNTTYTN	1860
QY	1861	GATGACTCAGGAGGCTCTCCACTCCGCGGCGACCCCGGAGCCGGGTGGAACGA	1920
Db	1861	GAYGNYTNCARGGNGNTGYWSNACNWSNCGNCGNMGNCNGCNGAYMNGTNGARMGN	1920
QY	1921	GTCAACCAAGCGCTGCGGTCCGCTCGGACAGCTGTACTTCTAGCTCGAAGCCCCAGGC	1980
Db	1921	GTNACNARGCNYTNMGNWSNCGNYTNGAYWSNTGYACNWSNWSNARGCNCNGN	1980
QY	1981	TGCTGCGAGGATGGGACCTGGGACCTGCACCTACACTAGAA	2022
Db	1981	TGYTGARGARTGGGAYTNGGNCNTGYACNACNYTNGAR	2022
RESULT 10			
BC004759			
LOCUS	Mus musculus interleukin 17 receptor C, mRNA (cdna clone MGC:6973		
DEFINITION	IMAGE:3154616), complete cds.		
ACCESSION	BC004759.1 GI:13435809		
VERSION	MG.		
KEYWORDS	Mus musculus (house mouse)		
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
1	(bases 1 to 2015)		
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,		
	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,		
	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,		
	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,		
	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,		
	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,		
	Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,		
	Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,		
	Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,		
	McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,		
	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,		
	Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,		
	Fahay, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S.,		
	Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,		
	Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,		
	Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,		
	Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,		
	Schmurch, A., Schein, J.E., Jones, S.J. and Maizra, M.A.		
	Generation and initial analysis of more than 15,000 full-length		
	human and mouse cDNA sequences		
	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
	12477932		
2	(bases 1 to 2015)		
	Strausberg, R.		
	Direct Submission		
	Submitted (21-MAR-2001) National Institutes of Health, Mammalian		

[illegible]

[illegible]

Db	1621	CAYGNGCNYTNGCTGGTTCAYCAYCARMGMNGMNATHYTNCARGGNGGNGTN	1680
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Db	1681	GTNATHYNTYNTYWSNCCNGCNGTNGCNCARTGYCARTGGYTNCARYTNCAR	1740
Qy	1669	ACAGTGGAGCCGGGCGGATAGACGCCCTTCGCGCTTGGCTAGCTAGCTGCCTACCGCAT	1728
Db	1741	ACNGTNGARCNGGNCNCAYGAYGNYTNGCNGCTGGYTWSNTYGYTNYTNCNGAY	1800
Qy	1729	TTTCCTCGAGGCGGGCGACCGCGCTACGTCGCGGTCTACTTCGACGGGCTGCTGCAC	1788
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Qy	1789	CCAGACTCTGTGCCCTCCCGGTCGCGCGCTCTTCTTCCCTCCGCGCAGCTG	1848
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Qy	1849	CCGGCTTTCGTGATGACTCGAGGAGGCTGCTCCACTTCCGCGGGCGACCGCGGAC	1908
Db	1921	CCNGCNTTYTNGAYGNYTNCARGNGGNTGWSNACNWSGNCNGNMGCCNGAY	1980
Qy	1909	CGGGTGAAACGAGTGAACCCAGGGCTCGGTCGCGCTCGAGACTGTACTTCTAGCTCG	1968
Db	1981	MNGTNGARMGNTNACNARGCNYTNGNWSGNCNTNGAYWSNTGYACNWSNWSN	2040
Qy	1969	GAAGCCCGAGGCTCTCGAGGAATGGGACTGGGACCTGGACCTGCACACTAGAA	2022
Db	2041	GARGCNCNGNTGYTGARGARTGGAYTNGGNCNTGYACNACNTNGAR	2094
RESULT 13			
CS251239		CS251239	2255 bp
LOCUS		Sequence 1 from Patent WO2005123778.	DNA
DEFINITION		CS251239	linear
ACCESSION		CS251239.1	PAT 18-JAN-2006
VERSION		GI:85361012	
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
		Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Presnell, S.R.	
TITLE		Soluble zcytor14, anti-zcytor14 antibodies and binding partners and methods of using in inflammation	
JOURNAL		Patent: WO 2005123778-A 1 29-DEC-2005;	
		ZymoGenetics, Inc. (US)	
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		KWVALVLAFLFAALSLILLKXDAKAAARGAALLYSADDSQFRLVGLGALS	
		LCQLPURAVDLWSRLEDSQAQFVAMFHQRQTLOEGSVNLLPSGPAVALCSEWL	
		DGVSGFGAGHPHDAFRASLSCVLPDLQGRAGTGVGACFDRLIHPDPAVPAFRTPV	
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ORIGIN

Query Match	57.5%	Score 1162.4	DB 2	Length 2255
Best Local Similarity	75.0%	Pred. No. 1.1e-280		
Matches 1541	Conservative 0	Mismatches 461	Indels 52	Gaps 5
Qy	1	ATGCTGTGTCCTGGTTCTGCTGCTCTGTGGCACTGGGCCGAAACCTCTGGTGGTCTCTCT	60	
Db	154	ATGCTGTGCTCTGGTTCTGCTGCTCTGTGGCACTGGGCCGAAACCTCTGGTGGTCTCTCT	213	
Qy	61	CTGAGAGACTGATGGAGCCTCAGACACTGCACGCTGCTCTCTAGGGCTCTCTGCGCAC	120	
Db	214	CTGAGAGGCTTGTGGGGCCTCAGAGAGCTACCACTGCTCTCGGGCCCTCTCTGCGCG	273	
Qy	121	CTCTGGGATGTTGACGTGCTCTGCTGCTGGAAAGCCTCCAGTCTGCCCCAGGCCCTGTG	180	
Db	274	CTCTGGGACAGTGACATACTCTGCTGCTGGGACATCGTGCCTGCTCGGGCCCGGTG	333	
Qy	181	CTAGTGCTACCCCTGCGAGAGCGAGTGTGTGAGGTGTGCACAGAGACAGATTGC	240	
Db	334	CTGGCGCTACGCACCTCGACACAGAGTGTGTGAGGTGCCAGAGAGACCGACTGT	393	
Qy	241	GCCCTCCGTGTCCTGTGGTGCACCTTGGCCGTGCATGGGACTGGGACAGCCGTAA	300	
Db	394	GACCTCTGTCTGCGTGTGGTGTCCACTTGGCCGTGCATGGGACTGGGAGAGCCGTAA	453	
Qy	301	GAAGCTGGAAAGT-----CTGATTTCAGAACTCCAGGAGTCTAGGAAAGCCCTCT	348	
Db	454	GATGAGGAAAGTTTGGGAGGACGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCT	513	
Qy	349	CTCAGGCCCHAGTGTGCTCTCTTCAGAGCCTTACCCTATCGCCCGTGTGCCCTGCTG	408	
Db	514	CTCAGGCCCAAGTGTGCTCTCTCTTCAGAGCCTTACCCTATCTGCCCGTGTGCCCTG	573	
Qy	409	GAGTCCAGGTGCCCGCTGACCTCGTGCAGCTCGTCACTCCGTGGTCTTCGCGGTATT	468	
Db	574	GAGTGCAGTGCCTCTGCCCCCTTGTGCAGTTTGGTCACTCTGTGGCTCTGTGTTATAT	633	
Qy	469	GACTGTTTCGAGGTAGTCTTTGGGGCTGAGTACAGATCTGGTCTCTACGAAAGCCAGG	528	
Db	634	GACTGCTTCGAGGTGCGCCTAGGAGTGAGGTACGAATCTGGTCTCTACTCAGCCCCAGG	693	
Qy	529	TACAGAAAGCTCAACCTCACACAGCAGTGCCT-----	564	
Db	694	TACAGAAAGAACTCAACACACACAGCAGCTGCTCCCTCGCTTCAGCTCAACGTGTCA	753	
Qy	565	---GATGGTGACAAATGCTCTTCACACTTGATGTCTCTGAGGAGCAGGACTTTAGCTTC	621	
Db	754	GCAGATGTTGACACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCTC	813	
Qy	622	TTACTGTACTCGCTCCAGTCCCGGATGCTCTCAAAATCCTTTGTGGTACAAAACCTGACT	681	
Db	814	TCCCTGTACTGGAAATCAGGTTCAGGGCCCCCAAAAGCCCGGTGGCACAAAACCTGACT	873	
Qy	682	GGACCTCAGAACATTACTTTAAACACACAGACCTGTTCCCTGCCCTCTGCATTACAGTG	741	
Db	874	GGACCGCAGATCATTAACCTTGAACACACAGACCTGGTTCCCTGCCCTCTGTATTACAGTG	933	
Qy	742	TGGTTCGCTAGAGCCAGACTCTGAGAGGGTTCGAAATTCCTGCCCTTCGGGAGAGATCCCGG	801	
Db	934	TGGCTCTTGGAACTGACTTCGTTTGGAGGAAATCTGCCCCCTTCAGGGAGACCCCGC	993	
Qy	802	GCAACACAGGAACCTCTGGCACAATAGCCAGGCTGCGGGTACTGTCTCCACAGGGGTATGCG	861	
Db	994	GCAACACAGGAACCTCTGGCAAGCCCGCACTGGCACTGTGCTGAGCCCTTCGAGAGCTGCTG	1053	
Qy	862	CTAGATGCGCTGTGCTGTGCCGGGCAAGGTAACTGTGCTGTGGCAGGCAACAGACAG	921	
Db	1054	CTGACGCAACGTTGCTCGCTGCCCGCAGAACGGGCACTGTGCTGTGGCGGCTCCGGGTGGG	1113	
Qy	922	AGTCCCTGCCAGCCACTTGTGTGCCACCAAGTGCCTCCAGAAAGACGCCACTGTGAATGAGCCA	981	
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QY	982	CAAGATTTCAGATTTGGTGGCAGGCCACCCCAAACCTCTGTGTCAGGTGACGCACCTGGGAG	1041
DB	1174	CTCAGATTTCCCATTGCTGTAAAGGCGACCCCTAAACCCTCTGTGTTTCAGSTGAACAGCTCGGAG	1233
QY	1042	AAGGTTTCAGCTGCAAGCGTGCTCGTGGGCTGACTCCCTTGGGGCCCTTCAAGGATGATATG	1101
DB	1234	AAGCTGCAGCTGCAGGAGTGCTTTGTGGGCTTGACTCCCTGGGGCCTCTCAAAGACGATGTG	1293
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QY	1342	TGCCTACTCTTGGCTGCGGGCGCTTTTCT TCTCTCTCTATAAAAAGGACCGCAGAGAA	1401
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QY	1402	GCGGCGGTGGCTCCCGCAGGGCTTGTCT CCTCCACTCCGCGACGAGCGGCTACGAG	1461
DB	1591	GCGGCCGCCAGGGGCGCGGGCTCTGCT CTCTACTCAGCCGATGACTCGGGTTTCGAG	1650
QY	1462	CGTCTGTTGGAGACACTGGCGTTCGCG GTTGAGCCAGATGCCTGCGCGTGGCGCTGGAC	1521
DB	1651	GCGCTGTTGGCGCCCTTGGCGTTCGG CCTGTGCCAGCTGCGCTGCGCTGGCGGTAGAC	1710
QY	1522	CTGTGGAGCCCGCGAGCTGAGCGCGCA CGGAGCCCTAGCCTGGTTTCCACCAACAGCGA	1581
DB	1711	CTGTGGAGCGCTCGTGAACCTGAGCG CGCAGGGGCCGTGGCTTGGTTTCA CGCGCAGCGG	1770
QY	1582	GCGCGTATCTGCAGAGGGTGGGCTGGT AAATCCTTCTCTCTCGCCGCGCGCGCTGGCG	1641
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QY	1642	CAGTGTTCAGCAGTGGCTGCA----- GCTCCAGACAGTGGAGCCCGGGCCGCATGAC	1692
DB	1831	CTGTGCAGCAGTGGCTACAGGATGGGG TGTCGGGCCCGGGCGCACGGCCCGCACGAC	1890
QY	1693	GCCCTCGCCCGCTGGCTCAGCTCGTG CTACCCGATTTCTGCAAGCGCGGGCGACCGCG	1752
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QY	1813	GCGGTGCCCGCTCTTCTCCCTGCCCA CAGCAGCTGCCGCTTTCTCTGGATGCACATGCAG	1872
DB	2011	GCGACCGTGGCGTCTTTCACACTG CCGCTCCCACTGCCAGACTTCTTGGGGGCCCTGCAG	2070
QY	1873	GGAGGCTGCTCCACTTCCGGGGGCGCA CCCCGGACCGGGTGGAAACAGATGCACCCAGGCG	1932
DB	2071	CAGCCTCGCGCCCGCTTCCGGGGGCT CCAAGAGAGAGCGGAGCAAGTGTCCCCGGGCC	2130
QY	1933	CTGCGGTCCGCGCTTGAGACAGCT- GTA CTTTAGCTCGGAAGCCCGCAGGCTGTCTCGGAGGA	1991
DB	2131	CTTCAGCCAGCCCTGGATAGTACTT CCAATCCCCCGGGGACTCCCGCGCCGAGACGCGGG	2190
QY	1992	ATGGGACTGGGAC	2005
DB	2191	GTGGGACGAGGGC	2204

RESULT 14	AX073993	2255 bp	DNA	linear	PAT 06-FEB-2001
LOCUS	Sequence 1 from Patent WO0104304.				
DEFINITION	AX073993				
ACCESSION	AX073993.1	GI:12710225			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1	Presnell, S.R., Burkhead, S.K. and Pownder, S.L.			
AUTHORS	Human cytokine receptor				
TITLE	Patent: WO 0104304-A.1 18-JAN-2001;				
JOURNAL	Zymogenetics, Inc (US)				
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	DILCLPGDIVPAGPVLAPLAPLHQLTELVRCKETDCDLRLVAHLAVHGHWEPEPDE				
	EKFGAADSVPVEPRNLSLOAVLSFQVPTARCVLVEQVPAALVQFGSVGVSY				
	DCFEAALGSVPRINSYTPRKEKLNLTQOLPALPLNVSADGNDVHLVILNYSVEQH				
	GLSLYNQVQVPPRPHKNTLGPQIITLANTDLVPCIQVWPLEPDSVRTNICPFR				
	EDPRAHNLWQAKRLTLTQSWLLDAPCSLPAEALCWAPGDDPCQLVPPLSWEN				
	VTVDKLEFFPLKHPNLVCVNSSEKLLQCEQLWADSLGPIKDDVLLLETGPODNR				
	SICALPEPGCTSLFSKASTRAARLGEYLLQLQSGCQLWDDDLGALWACPMDKYIH				
	KRWALVWLACILFLAAALSILILLKKDHAKAARGAALLLYLSADDSFERLVGALISA				
	LCOLPLRVAVDLWRRELSSAQPVAFWHAQRQTLOEGVVVILLFSPGVALCSWQL				
	DGVSGPAHGPHDAFRASLSCVLPFLQGRAPGSYGACFDRLHHPDAVPALPRTVPV				
	RTLPSQLPDFLQALQOPRAPRSRGLQERAQEQVSRLQALDYSVFHPPEGTPAPGRGVGP				
	GATPGAGDGT"				
ORIGIN					
Query Match	57.5%;	Score 1162.4;	DB 2;	Length 2255;	
Best Local Similarity	75.0%;	Pred. No. 1.1e-280;			
Matches 1541; Conservative	0;	Mismatches 461;	Indels	52; Gaps	5;
QY	1	ATGCCTGTGTCTGGTTCCTGTCTGTGGCAGCTGGCCGAAACCCCTGTGTGTCTCT	60		
DB	154	ATGCCTGTGCCCTGGTTCCTGTCTGTGGCAGCTGGCCGAAACCCAGTGTCTTCT	213		
QY	61	CTGGAGAGACTGATGAGAGCCTCAGGACACTGCAGCCTGTCTTAGGCTCTCTCTGCCAC	120		
DB	214	CTGGAGAGCCTGTGGGGCCTCAGGAGCTACCCACTGTCTCCGGGCTCTCTCTGCCGC	273		
QY	121	CTCTGGGATGGTGAACGTCTCTGCTGCTGMAAGCTCCAGTCTGCCCGCCAGCCCTCTG	180		
DB	274	CTCTGGGACAGTGACATACTCTGCTGCTGGGACATCGTGCCTGTCTCCGGCCCCCGTG	333		
QY	181	CTAGTGCCTACCCGCTCGACGAGCGAGCTGTGTCTGAGTGTCTCAGTGTCTCAGAAACA	240		
DB	334	CTGGCGCTTACGACACCTGACAGAGCTGGTGTCTGAGTGTCTCAGAAAGAGACCACTGT	393		
QY	241	GCCCTCCGTCTCCGTGTGGTGTCCATCTGGCCGCTGCATGGGACCTGGCGACAGCTGAA	300		
DB	394	GACCTCTGTCTGGTGTGGTGTCCATCTGGCCGCTGCATGGGACCTGGGAAAGACCTGAA	453		
QY	301	GAAGCTGGAAGT-----CTGATTCAAGACTCCAGGAGTCTTAGGAACGCCTCT	348		
DB	454	GATAGGAAAAAGTTTGAGGAGCAGCTGACTCAGGGGTGGAGGAGCTAGGAATGCTCTCT	513		
QY	349	CTCCAGGCCAGGTGGTGTCTCTCTTCCAGGCTTACCCATCCCGCTGTGCTGCTGCTG	408		

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QY	1102	CTGTTAGTGGAGATGAACCGCCTCAACAACATCATGTCGTGTGCCTTTGGAAACCAGT	1161
DB	1373	CTACTGTTGGAGACAGAGCCCCCAGGACAACAGATCCCTCTGTGCTTTGGAAACCAGT	1432
QY	1162	GGCTGTACACCACTGCCAGCATGGCCTCACAGAGAGCTGCTCCCTTGGGAGAGGAGTTG	1221
DB	1433	GGCTGTACTTCACTACCCAGCAAAGCCTCCAGAGGAGCTCCGCTTGAGAGTAGTACTTA	1492
QY	1222	CTGCAAGACTTCGATGATCACAGAGTGATGCAAGCTGTGAAACGATGACAACTGGGATCG	1281
DB	1493	CTACAAGACTTCGAGTCAAGCCAGTGTCTGCAAGCTATGGACGATG---ACTTGGGAGCG	1549
QY	1282	CTATGGSCCTGCCCATGGACAAGTACATCCAAGCGCTGGGTCCTTAGTATGCTGGCC	1341
DB	1550	CTATGGGCTTGCCCATGGACAAATAATATCCAAGCGCTGGGCCCTCGTGTGGCTGGCC	1609
QY	1342	TGCCTACTCTTGGCTGGGGCGCTTTCTTCTTCTTCTTCTTAAAAGAACCGCAGGAAA	1401
DB	1610	TGCCTACTCTTGGCGCTGGCGCTTCCCTCATCTCTCTTCTCAAAGAAGATCACCGGAAA	1669
QY	1402	-----GCGGCCCGCTGGCTCCGCGACG	1422
DB	1670	GGGTGGCTGAGGCTTTGAAACAGGAGCTCCGCTCGGGGCGCGCCAGGGGCGCGCG	1729
QY	1423	GCTTGTCTCTTCCATCTCGCGCAGCGAGCGGGCTTACGAGGCTCTGGTGGGAGCACTGGCG	1482
DB	1730	GCTCTGCTCTTACTACTCAGCCGATGACTCTGGGTTTTGAGGCGCTGGTGGGGCGCCCTGGCG	1789
QY	1483	TCCGCTGTAGCCAGATGCCACTCTGGCGTGGCGTGACCTGTGAGACCGCGCGCAGCTG	1542
DB	1790	TGGGCGCTGTGCCAGCTGCCCTCGCGTGGCGTAGACCTGTGAGACCGCTCGTGAACCTG	1849
QY	1543	ACGGCGCAGGAGCCCTAGCTGTGTCCACCAACAGCGACCGCGTATCTGTGAGAGGGT	1602
DB	1850	AGCGGCGAGGGGCCCTGGCTTGGTTTACGCGCAGCGCGCCAGACCCCTGCAGGAGGGC	1909
QY	1603	GGCGTGTAAATCCCTTCTCTTCGCGCGCGCGCTGGCGCAGTGTCAAGCAGTGGCTGCA-	1661
DB	1910	GGCGTGTGTCTTGCTCTTCTCTCCCCTGGTGGCTGTGTCAGCAGTGGCTTACAG	1969
QY	1662	-----GCTCGACAGACTGAGCCCGGGCGGATACGCCCTCGCGCGCTGGCTCAGC	1713
DB	1970	GATGGGGTGTCCGGGCGCGGGCGCACCGGCCCGCGACGCTACGTGGGGGCTCGTTC	2089
QY	1714	TGCGTGTATTCCCGAATTCCTGCAAGCGCGGGCGAACCGCGCTACGTGGGGTCTACTTC	1773
DB	2030	TGCGTGTCTGCCGACTTCTTGACGGGCGGGCGCCCGGACGCTACGTGGGGGCTCGTTC	2089
QY	1774	GACGGGTGTGACCCAGACTGTGTCCTCCCGTTCCCGTTCGCGTCCCGCTCTTCTCC	1833
DB	2090	GACAGGTGTCTCACCCGAGCCGCTACCCGCCCTTTTCCGACGCTGGCGCTCTTACAC	2149
QY	1834	CTGCCACGAGCTGCGCGCTTCTCTGGATGCACTGCAAGGAGGCTGCTCCACTTTCGCG	1893
DB	2150	CTGCCCTTCCCACTTGCCAGACTTCTTGGGGGCCCTGACAGAGCTTCGCGGCCCGCTTC	2209
QY	1894	GGGCGACCCGCGGACCGGGTGGAAACAGTGAACAGGCGCTCGGTTCGCGCTCGACAGC	1953
DB	2210	GGGCGGCTTCAAAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACGCCAGCCCTGGATAGC	2269
QY	1954	T-GTACTTCTAGCTCGGAAGCCAGGCTGCTCGAGGAAATGGGACCTGGGAC	2005
DB	2270	TACTTCAATCCCCGGGGAATCCCCGCGCGGAGCGCGGGTGGGACGAGGCGC	2322

Search completed: August 17, 2006, 00:32:23
Job time : 11541 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 20:57:35 ; Search time 1330 Seconds
(without alignments)
10599.915 Million cell updates/sec

Title: US-10-719-202-1_COPY_197_2218
Perfect score: 2022
Sequence: 1 atgcctgtctcgtctct.....gaccctgcactacactagaa 2022

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005as:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				SUMMARIES	
Result No.	Score	Query Match	Length DB	ID	Description
1	2022	100.0	2256	6	Aad24220 Murine cy
2	1980.2	97.9	2269	15	Aef05372 Murine zcy
3	1962.2	97.0	2287	15	Aef05376 Murine zcy
4	1940	95.9	2328	6	Aad24222 Murine cy
5	1933.6	95.6	2328	6	Aad24222 Murine cy
6	1933.6	95.6	2314	6	Aad24222 Murine cy
7	1933.6	95.6	2314	14	Aad24222 Murine cy
8	1929.6	95.4	2331	6	Aad24221 Murine cy
9	1412.2	69.8	2022	6	Aad24221 Murine cy
10	1330.2	65.8	2094	6	Aad24223 Murine cy
11	1327.6	65.7	2094	6	Aad24223 Murine cy
12	1162.4	57.5	2255	4	Aad24223 Murine cy
13	1162.4	57.5	2255	10	Aad24223 Murine cy
14	1162.4	57.5	2255	15	Aad24223 Murine cy
15	1113.4	55.1	2380	4	Aad24223 Murine cy
16	1113.4	55.1	2380	4	Aad24223 Murine cy
17	1113.4	55.1	2380	4	Aad24223 Murine cy
18	1113.4	55.1	2380	6	Aad24223 Murine cy

19	1113.4	55.1	2380	6	ABL88253	Ab188253 Human PRO
20	1113.4	55.1	2380	6	ABL95742	Ab195742 Human ang
21	1113.4	55.1	2380	8	ACA89673	ACA89673 cDNA enco
22	1113.4	55.1	2380	8	ACA73683	ACA73683 Human sec
23	1113.4	55.1	2380	8	ACA05998	ACA05998 Human sec
24	1113.4	55.1	2380	8	ACA66832	ACA66832 cDNA enco
25	1113.4	55.1	2380	8	ACA91244	ACA91244 Novel hum
26	1113.4	55.1	2380	8	ACD81621	ACD81621 Human CDN
27	1113.4	55.1	2380	8	ACF20407	ACF20407 Human sec
28	1113.4	55.1	2380	8	ACF19793	ACF19793 Human sec
29	1113.4	55.1	2380	8	ACD22081	ACD22081 Human sec
30	1113.4	55.1	2380	8	ACF13246	ACF13246 Human sec
31	1113.4	55.1	2380	8	ACD25349	ACD25349 Human sec
32	1113.4	55.1	2380	8	ACF00398	ACF00398 Human sec
33	1113.4	55.1	2380	8	ACA60443	ACA60443 Novel hum
34	1113.4	55.1	2380	8	ACA72455	ACA72455 Novel hum
35	1113.4	55.1	2380	8	ACD04979	ACD04979 Novel hum
36	1113.4	55.1	2380	8	ACD18440	ACD18440 Human sec
37	1113.4	55.1	2380	8	ACD08447	ACD08447 Human sec
38	1113.4	55.1	2380	8	ACA88881	ACA88881 Novel hum
39	1113.4	55.1	2380	8	ACA70323	ACA70323 Human sec
40	1113.4	55.1	2380	8	ACD12545	ACD12545 Novel hum
41	1113.4	55.1	2380	8	ACC74460	ACC74460 Human sec
42	1113.4	55.1	2380	8	ACD16088	ACD16088 Human sec
43	1113.4	55.1	2380	8	ACD25656	ACD25656 Novel hum
44	1113.4	55.1	2380	8	ACD18133	ACD18133 Human sec
45	1113.4	55.1	2380	8	ACC88420	ACC88420 Human sec

ALIGNMENTS

RESULT 1
AAD24220
ID AAD24220 standard; DNA; 2256 BP.

AC AAD24220;

XX 17-MAY-2002 (first entry)

XX Murine cytokine receptor Zcytor14 DNA.

XX Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
XX gene therapy; protein therapy; gene; ds.

OS Mus sp.

XX Key Location/Qualifiers
XX CDS 197..2221

FT /*tag= a
FT /product= "Cytokine receptor, Zcytor14"
FT sig_peptide 197..256
FT /*tag= b

FT mat_peptide 257..2218
FT /*tag= c

FT /product= "Mature cytokine receptor, Zcytor14"

XX WO200204519-A2.

XX 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US021344.

XX 06-JUL-2000; 2000US-0216446P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gao Z;

XX WPI; 2002-179701/23.

XX P-PSDB; AAE14559.

XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the

receptor, useful for treating inflammation, specifically rheumatoid arthritis, and as educational tools or in research.

Claim 8; Page 87-90; 99pp; English.

The present sequence is murine cytokine receptor Zcytor14 DNA. The Zcytor14 polypeptide is useful for identifying or isolating Zcytor14 ligands, in preparing antibodies, in identifying proteins or peptide cleavage sites, in amino acid sequence analysis, and in monitoring biological activities of both the native and tagged protein in vitro or in vivo. Polypeptides having Zcytor14 activity can be used to treat inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational tool in genetics, molecular biology, protein chemistry and antibody production analysis, in the preparation of expression constructs for bacterial, viral or mammalian expression, in determining mRNA and DNA localisation of Zcytor14 polynucleotide in tissues, for identifying related polynucleotides and polypeptides by nucleic acid hybridisation, in linkage-based testing for various diseases in murine models, and to determine whether a subject's chromosomes contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo diagnosis, and for detecting and localising Zcytor14 gene expression in tissue samples

Sequence 2256 BP; 416 A; 706 C; 679 G; 455 T; 0 U; 0 Other;

Query Match		100.0%;	Score 2022;	DB 6;	Length 2256;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2022;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCCCTGCTCCTGGTTCCTGCTGCTGCTGGCACTGGGCGGAAACCTGTGCTCTCT	60		
DB	197	ATGCCCTGCTCCTGGTTCCTGCTGCTGCTGGCACTGGGCGGAAACCTGTGCTCTCT	256		
QY	61	CTGGAGAGACTGATGAGGCTCAGGACACTGCACTGCTCTCTAGGCTCTCTCTGCGCAC	120		
DB	257	CTGGAGAGACTGATGAGGCTCAGGACACTGCACTGCTCTCTAGGCTCTCTCTGCGCAC	316		
QY	121	CTCTGGATGCTGAGCTGCTGCTGCTGCTGGAGCCTCAGTCTGCTGCTGCTGCTGCTG	180		
DB	317	CTCTGGATGCTGAGCTGCTGCTGCTGCTGGAGCCTCAGTCTGCTGCTGCTGCTGCTG	376		
QY	181	CTAGTGCCTACCGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240		
DB	377	CTAGTGCCTACCGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	436		
QY	241	GCCTCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300		
DB	437	GCCTCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	496		
QY	301	GAAGCTGGAAGTCTGATTCAGAACTCCAGAGCTTAGGAAGCCTCTCTCCAGGCGCCAG	360		
DB	497	GAAGCTGGAAGTCTGATTCAGAACTCCAGAGCTTAGGAAGCCTCTCTCCAGGCGCCAG	556		
QY	361	GTGCTGCTCTCTTCCAGGCTTACCCCATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420		
DB	557	GTGCTGCTCTCTTCCAGGCTTACCCCATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	616		
QY	421	CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480		
DB	617	CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	676		
QY	481	GCTAGTCTTGGGCTGAGGTACAGATCTGCTCTACAGAGCCAGGTACCAAGAAAGAG	540		
DB	677	GCTAGTCTTGGGCTGAGGTACAGATCTGCTCTACAGAGCCAGGTACCAAGAAAGAG	736		
QY	541	CTCAACCTTCACACAGCAGCTGCTGATGGTGAACATGCTCTTCTGACACTGGATGCTCT	600		
DB	737	CTCAACCTTCACACAGCAGCTGCTGATGGTGAACATGCTCTTCTGACACTGGATGCTCT	796		
QY	601	GAGAGCAGGACTTTAGCTTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660		
DB	797	GAGAGCAGGACTTTAGCTTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	856		

QY	661	TTCTGCTACAAAAACCTGACTGGACCTCAGAACATTTAAACACACAGACCTGGTT	720
DB	857	TTCTGCTACAAAAACCTGACTGGACCTCAGAACATTTAAACACACAGACCTGGTT	916
QY	721	CCCTGCTCTGCAATTCAGGTGCTGCTAGAGCCAGACTCTGAGAGGTCGAATTCCTGC	780
DB	917	CCCTGCTCTGCAATTCAGGTGCTGCTAGAGCCAGACTCTGAGAGGTCGAATTCCTGC	976
QY	781	CCCTTCGGGAAGATCCCGGTGCACAGGAACCTCTGGCACATAGCCAGGCTGCCGGTA	840
DB	977	CCCTTCGGGAAGATCCCGGTGCACAGGAACCTCTGGCACATAGCCAGGCTGCCGGTA	1036
QY	841	CTGTCCCCAGGGGTATGGCAGCTAGATGCGCCTTGTCTGTGCTGCGGCAAGTAACACTG	900
DB	1037	CTGTCCCCAGGGGTATGGCAGCTAGATGCGCCTTGTCTGTGCTGCGGCAAGTAACACTG	1096
QY	901	TGCTGGCAGGACCCAGACAGTCCCTGCGCAGCCTTGTGTCACAGGTCACAGGCCCCAGAAG	960
DB	1097	TGCTGGCAGGACCCAGACAGTCCCTGCGCAGCCTTGTGTCACAGGTCACAGGCCCCAGAAG	1156
QY	961	AACGCCACTGTGAATGAGCCACAGATTTCCAGTTGCTGGCAGGCCACCCCAACCTCTGT	1020
DB	1157	AACGCCACTGTGAATGAGCCACAGATTTCCAGTTGCTGGCAGGCCACCCCAACCTCTGT	1216
QY	1021	GTCCAGGTGAGCACCTCGGAGAGGTTTCACTGCAAGCTGCTGCTGGGCTGACTCCTTG	1080
DB	1217	GTCCAGGTGAGCACCTCGGAGAGGTTTCACTGCAAGCTGCTGCTGGGCTGACTCCTTG	1276
QY	1081	GGGGCTTCAAGATGATATGCTTGTAGTGGAGATGAAAACCGGCTCAACAAACATCA	1140
DB	1277	GGGGCTTCAAGATGATATGCTTGTAGTGGAGATGAAAACCGGCTCAACAAACATCA	1336
QY	1141	GTCTGTGCTTGGAAACCCAGTGGCTGTACACACTGCTCCAGCATGGCTCCACAGAGCT	1200
DB	1337	GTCTGTGCTTGGAAACCCAGTGGCTGTACACACTGCTCCAGCATGGCTCCACAGAGCT	1396
QY	1201	GCTCGCTGGGAGAGGATTCCTGCAAGACTTCCGATCACCAGTGTATCAGCTGTGG	1260
DB	1397	GCTCGCTGGGAGAGGATTCCTGCAAGACTTCCGATCACCAGTGTATCAGCTGTGG	1456
QY	1261	AACGATGACACATGAGGATTCCTATGGGCTGCTGCTGCAAGTATCATCCACAGGCGC	1320
DB	1457	AACGATGACACATGAGGATTCCTATGGGCTGCTGCTGCAAGTATCATCCACAGGCGC	1516
QY	1321	TGGGCTCTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380
DB	1517	TGGGCTCTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1576
QY	1381	CTAAAAAGGACCCGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1440
DB	1577	CTAAAAAGGACCCGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1636
QY	1441	GCCGAGGAGCGGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1500
DB	1637	GCCGAGGAGCGGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1696
QY	1501	CCACTGCGCTGGGCTGGAACCTGTGAGAGCCCGGCTGAGCGCGGAGCCCTA	1560
DB	1697	CCACTGCGCTGGGCTGGAACCTGTGAGAGCCCGGCTGAGCGCGGAGCCCTA	1756
QY	1561	GCTGCTTCCACACAGGAGCCGCTATCCCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG	1620
DB	1757	GCTGCTTCCACACAGGAGCCGCTATCCCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG	1816
QY	1621	TTCTCCCGCGCGGCTGCGCAGTGTACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1680
DB	1817	TTCTCCCGCGCGGCTGCGCAGTGTACAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1876
QY	1681	GGGCGGATGACCGCTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
DB	1877	GGGCGGATGACCGCTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1936
QY	1741	CGGGCGAGCGGCGCTACCTGCGGGCTTACTTTCGACGCGGCTGCTGCTGCTGCTGCTGCTG	1800

Db 1937 CGGGCGACCGCGCTACGTCGGGGTCTACTTGCACGGGCTGCTGCACCCAGACTCTGTG 1996
 Qy 1801 CCTCTCCCGTTCGCGCTGCGCCCGCTCTTCTCCCTGCCACGAGCTGCGCGCTTTCCTG 1860
 Db 1997 CCTCTCCCGTTCGCGCTGCGCCCGCTCTTCTCCCTGCCACGAGCTGCGCGCTTTCCTG 2056
 Qy 1861 GATGCACTGACGAGGCTGCTGCATTCGCGGGGGGAGCCCGGACCGGGTGGAAACGA 1920
 Db 2057 GATGCACTGACGAGGCTGCTGCATTCGCGGGGGGAGCCCGGACCGGGTGGAAACGA 2116
 Qy 1921 GTGACCCAGGCGCTGCGGTCGCGCTCGGACAGCTGTACTTCTAGCTCGGAAGCCCGCAGGC 1980
 Db 2117 GTGACCCAGGCGCTGCGGTCGCGCTCGGACAGCTGTACTTCTAGCTCGGAAGCCCGCAGGC 2176
 Qy 1981 TGCTGCGAGGAATGGGACCTGGGACCTGCACTACACTAGAA 2022
 Db 2177 TGCTGCGAGGAATGGGACCTGGGACCTGCACTACACTAGAA 2218
 RESULT 2
 AEF05372
 ID AEF05372 standard; cDNA; 2269 BP.
 XX AEF05372;
 AC AEF05372;
 DT 23-FEB-2006 (first entry)
 XX Mouse zcytor14 variant cDNA SEQ ID NO 25.
 XX antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
 KW antiarthritic; dermatological; antipsoriatic; antibacterial;
 KW immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
 KW inflammatory bowel disease; asthma; respiratory disease;
 KW ulcerative colitis; antiulcer; Crohn's disease; gastrointestinal-gen.;
 KW gastrointestinal disease; arthritis; antipsoriatic;
 KW musculoskeletal disease; psoriasis; antipsoriatic;
 KW dermatological disease; immune disorder; atopic dermatitis;
 KW dermatological; endotoxemia; inflammation; endotoxemic shock; sepsis;
 KW antibacterial; immunosuppressive; infection; zcytor14; mutant;
 KW coding sequence; ss.
 OS Mus musculus.
 XX
 XX
 FH Key Location/Qualifiers
 FT 197..2248
 CDS /*tag= a
 FT /*product= "Mouse zcytor14 variant "
 FT
 XX
 PN W02005123778-A2.
 XX
 PD 29-DEC-2005.
 XX
 PP 10-JUN-2005; 2005WO-US020521.
 XX
 PR 10-JUN-2004; 2004US-0578805P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 PA Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
 PI Jaspers SR, Billaborough J;
 XX
 XX WPI; 2006-067457/07.
 DR P-PSDB; AEF05373.
 XX
 PT New isolated soluble receptor comprises at least one Zcytor14 subunit,
 PT useful for treating an inflammatory disease, e.g. asthma, inflammatory
 PT bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
 PT psoriasis.
 XX
 PS Example 28; SEQ ID NO 25; 205pp; English.
 XX
 CC The invention describes an isolated soluble receptor comprises at least

CC one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
 CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
 CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
 CC ID NO. 24) given in the specification. Also described are: an isolated
 CC soluble receptor comprising Zcytor14, where Zcytor14 comprises a
 CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
 CC the pro-inflammatory activity of either IL-17A comprising fully defined
 CC 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
 CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
 CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
 CC and where the antibody or antibody fragment reduces the pro-inflammatory
 CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
 CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
 CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
 CC role; and treating a pathological condition in a subject associated with
 CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
 CC subunit is useful for treating an inflammatory disease, e.g. asthma;
 CC chronic inflammatory disease selected from inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
 CC psoriasis; or acute inflammatory disease selected from endotoxemia,
 CC septicemia, toxic shock syndrome, or infectious disease. This sequence
 CC represents a mouse IL-17A and IL-17F receptor zcytor14 variant.
 XX
 SQ Sequence 2269 BP; 405 A; 713 C; 685 G; 466 T; 0 U; 0 Other;
 Query Match 97.9%; Score 1980.2; DB 15; Length 2269;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 2019; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
 QY 1 ATGCCGTGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 DB 197 ATGCCGTGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256
 QY 61 CTGGAGAGACTGATGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGG 120
 DB 257 CTGGAGAGACTGATGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGG 316
 QY 121 CTCTGGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 317 CTCTGGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376
 QY 181 CTAGTGCCTTACCCGCTGCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 DB 377 CTAGTGCCTTACCCGCTGCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
 QY 241 GCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 DB 437 GCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
 QY 301 GAACTGGAAAGTCTGATTCAGAACTCCAGGAGTCTAGGAACTGCTTCTTCCAGGCCAG 360
 DB 497 GAACTGGAAAGTCTGATTCAGAACTCCAGGAGTCTAGGAACTGCTTCTTCCAGGCCAG 556
 QY 361 GTGGTGTCTCTCTCCAGGCTTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 DB 557 GTGGTGTCTCTCTCCAGGCTTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
 QY 421 CCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 617 CCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
 QY 481 GCTAGTCTTGGGGCTGAGGTACAGATCTGGTCTTACAGAACTGCTTCTTCCAGAAAGAG 540
 DB 677 GCTAGTCTTGGGGCTGAGGTACAGATCTGGTCTTACAGAACTGCTTCTTCCAGAAAGAG 736
 QY 541 CTCACCTCTCACACAGCAGCTGCT-----GATGCTGAC 573
 DB 737 CTCACCTCTCACACAGCAGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
 QY 574 AATGTCCTTCTGACACTGGATGTCTCTGAGGAGCAGGACTTTAGCTTTCTTACTGTACCTG 633
 DB 797 AATGTCCTTCTGACACTGGATGTCTCTGAGGAGCAGGACTTTAGCTTTCTTACTGTACCTG 856

[illegible]

Db	1937	TGCGTGACCGATTCTCTGCAAGCCGGGACCGGCCGTACATCGGGGCTACTTC	1996
QY	1774	GACGGGCTGTCACCCAGACTCTGTGCCCTCCCGTTCGGGTTCGCCCGGTCTTCTTC	1833
Db	1997	GACGGGCTGCTGCACCCAGACTCTGTGCCCTCCCGTTCGGGTTCGCCCGGTCTTCTTC	2056
QY	1834	CTGCCACACAGCTGCCGCTTTCCTGGATGCAATGCAAGGAGGTCTTCACTTCGGCG	1893
Db	2057	CTGCCCTCGCAGTCCGCGCTTTCCTGGATGCAATGCAAGGAGGTCTTCACTTCGGCG	2116
QY	1894	GCGCGACCCGCGACCGGCTGGAAACAGATGACCCAGCGCTCGCGTCCGCCCTGGACAGC	1953
Db	2117	GCGCGACCCGCGACCGGCTGGAAACAGATGACCCAGCGCTCGCGTCCGCCCTGGACAGC	2176
QY	1954	TGTACTTCTAGTTCGGAAGCCCGAGGCTGTTCGAGGAATGGAGCTGGACCTTGCACT	2013
Db	2177	TGTACTTCTAGTTCGGAAGCCCGAGGCTGTTCGAGGAATGGAGCTGGACCTTGCACT	2236
QY	2014	ACACTAGAA	2022
Db	2237	ACACTAGAA	2245
RESULT 3			
AEF05376	ID AEF05376 standard; cDNA; 2287 BP.		
XX	AC	AEF05376;	
XX	AC	23-FEB-2006 (first entry)	
XX	DE	Mouse zcytoR14 variant cDNA SEQ ID NO 29.	
XX	KW	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;	
XX	KW	antiarthritic; dermatological; antipsoriatic; antibacterial;	
XX	KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;	
XX	KW	inflammatory bowel disease; asthma; respiratory disease;	
XX	KW	ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;	
XX	KW	gastrointestinal disease; arthritis; antiarthritic;	
XX	KW	musculoskeletal disease; psoriasis; antipsoriatic;	
XX	KW	dermatological disease; immune disorder; atopic dermatitis;	
XX	KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;	
XX	KW	antibacterial; immunosuppressive; infection; zcytoR14; mutant;	
XX	KW	coding sequence; ss.	
XX	OS	Mus musculus.	
XX	FH	Key Location/Qualifiers	
FT	CDS	197..2266	
FT	FT	/*tag= a	
FT	FT	/product= "Mouse zcytoR14 variant"	
XX	PN	WO2005123778-A2.	
XX	PD	29-DEC-2005.	
XX	PF	10-JUN-2005; 2005WO-US020521.	
XX	PR	10-JUN-2004; 2004US-0578905P.	
XX	PA	(ZYMO) ZYMOGENETICS INC.	
XX	PI	Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;	
XX	PI	Jaspers SR, Billsborough J;	
XX	XX	WPI; 2006-067457/07.	
DR	DR	P-PSDB; AEF05377.	
XX	XX	New isolated soluble receptor comprises at least one zcytoR14 subunit,	
PT	PT	useful for treating an inflammatory disease, e.g. asthma, inflammatory	
PT	PT	bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or	
PT	PT	psoriasis.	

XX Disclosure; SEQ ID NO 29; 205pp; English.

XX The invention describes an isolated soluble receptor comprises at least

XX one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide

CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises

CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ

CC ID NO. 24) given in the specification. Also described are: an isolated

CC soluble receptor comprising Zcytor14, where the Zcytor14 comprises a

CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces

CC the pro-inflammatory activity of either IL-17A comprising fully defined

CC 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153

CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds

CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 21,

CC and where the antibody or antibody fragment reduces the pro-inflammatory

CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);

CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal

CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a

CC role; and treating a pathological condition in a subject associated with

CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14

CC subunit is useful for treating an inflammatory disease, e.g. asthma;

CC chronic inflammatory disease selected from inflammatory bowel disease,

CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or

CC psoriasis; or acute inflammatory disease selected from endotoxemia,

CC septicemia, toxic shock syndrome, or infectious disease. This sequence

CC represents a mouse IL-17A and IL-17F receptor Zcytor14 variant.

XX

SQ Sequence 2287 BP; 410 A; 715 C; 696 G; 466 T; 0 U; 0 Other;

Query Match 97.0%; Score 1962.2; DB 15; Length 2287;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2019; Conservative 0; Mismatches 3; Indels 45; Gaps 1;

QY 1 ATGCTGTGTCTGTTCTCTGCTGCTCTGGCACTGGCCGGAACCTGTGTCGTCTCT 60

DB 197 ATGCTGTGTCTGTTCTCTGCTGCTCTGGCACTGGCCGGAACCTGTGTCGTCTCT 256

QY 61 CTGGAGAGACTGATGAGGCTCTAGGACATCGACAGCTGCTCTTAGGCTCTCTCTGCCAC 120

DB 257 CTGGAGAGACTGATGAGGCTCTAGGACATCGACAGCTGCTCTCTAGGCTCTCTCTGCCAC 316

QY 121 CTCTGGAGAGTGTGACCTGCTCTGCTGCTGCTGGAGGCTCTCAAGTCTGCTGCTGCTG 180

DB 317 CTCTGGAGAGTGTGACCTGCTCTGCTGCTGCTGGAGGCTCTCAAGTCTGCTGCTGCTG 376

QY 181 CTAGTGTCTTACCCGCTCTGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

DB 377 CTAGTGTCTTACCCGCTCTGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436

QY 241 GCGCTCGGTGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

DB 437 GCGCTCGGTGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496

QY 301 GAAGCTGGAAAGTCTGATTCAGAACTCCAGAGTCTAGGAAGCTCTCTCCAGGCTGCTG 360

DB 497 GAAGCTGGAAAGTCTGATTCAGAACTCCAGAGTCTAGGAAGCTCTCTCCAGGCTGCTG 556

QY 361 GTGGTGTCTCTCTTCCAGGCTTACCCATCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

DB 557 GTGGTGTCTCTCTTCCAGGCTTACCCATCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616

QY 421 CCCGCTGACCTGTGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

DB 617 CCCGCTGACCTGTGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676

QY 481 GCTAGTCTTGGGCTGAGGTACAGATCTGCTCTACAGAGCCGAGGTACCAAGAGAG 540

DB 677 GCTAGTCTTGGGCTGAGGTACAGATCTGCTCTACAGAGCCGAGGTACCAAGAGAG 736

QY 541 CTCAACTCTACACAGAGCTGCT 564

DB 737 CTCAACTCTACACAGAGCTGCT 796

QY 565 -----GATGGTGA CAATGTCTCTTGACACATGGATGTCTCTGAGAGCAGGACTTTT 615

DB 797 AGCTGCTGGATGGTGA CAATGTCTCTTGACACATGGATGTCTCTGAGAGCAGGACTTTT 856

QY 616 AGCTTCTTACTCTACTCGTCCAGTCCCGGATGCTCTCAAAATCCTTGTGGTACAAAAC 675

DB 857 AGCTTCTTACTCTACTCGTCCAGTCCCGGATGCTCTCAAAATCCTTGTGGTACAAAAC 916

QY 676 CTGACTGGACCTCAGAACATTAATTTAAACCAACAGACCTGGTTCCTCTGCAAT 735

DB 917 CTGACTGGACCTCAGAACATTAATTTAAACCAACAGACCTGGTTCCTCTGCAAT 976

QY 736 CAGGTGTGTCTCTAGAGCCAGACTCTGAGAGGTGCAATTTCTGCCCCCTTCGGGAGAT 795

DB 977 CAGGTGTGTCTCTAGAGCCAGACTCTGAGAGGTGCAATTTCTGCCCCCTTCGGGAGAT 1036

QY 796 CCCGTGACACAGAACTCTGGCACATAGCACAGCTGCGGTACTGTCTCCACAGGGTA 855

DB 1037 CCCGTGACACAGAACTCTGGCACATAGCACAGCTGCGGTACTGTCTCCACAGGGTA 1096

QY 856 TGGCAGCTAGATGCGCTTGTCTCTGCGGGCAAGGTAAACATGTGTGCGGAGGCCA 915

DB 1097 TGGCAGCTAGATGCGCTTGTCTCTGCGGGCAAGGTAAACATGTGTGCGGAGGCCA 1156

QY 916 GACAGAGTCTCTGACGACCTTGTGCAACAGTGCCTCCAGAGAAACGCTCTGTGAAT 975

DB 1157 GACAGAGTCTCTGACGACCTTGTGCAACAGTGCCTCCAGTGCCTCCAGAGAAACGCTCTGTGAAT 1216

QY 976 GAGCCACAAGATTTCCAGTTGGTGCAGGCCACCCAACTCTGTGTCCAGGTGAGCAC 1035

DB 1217 GAGCCACAAGATTTCCAGTTGGTGCAGGCCACCCAACTCTGTGTCCAGGTGAGCAC 1276

QY 1036 TGGGAGAAAGTTTCACTGCAAGCTGCTGCTGGGCTGACTCTCTTGGGGCTTCAAGAT 1095

DB 1277 TGGGAGAAAGTTTCACTGCAAGCTGCTGCTGGGCTGACTCTCTTGGGGCTTCAAGAT 1336

QY 1096 GATATGCTTGTAGTGGAGATGA AAAACCGGCTCTAAACAACATCATGTGTGCTGCTG 1155

DB 1337 GATATGCTTGTAGTGGAGATGA AAAACCGGCTCTAAACAACATCATGTGTGCTGCTG 1396

QY 1156 CCCAGTGGCTGTACACCACTGCCAGCATGGCTCCACAGAGCTGCTGCTGCTGAGAG 1215

DB 1397 CCCAGTGGCTGTACACCACTGCCAGCATGGCTCCACAGAGCTGCTGCTGCTGAGAG 1456

QY 1216 GAGTTGCTGCAAGACTTCCGATCAACCAAGTGTATGCAAGCTGTGGAACGATGCAACATG 1275

DB 1457 GAGTTGCTGCAAGACTTCCGATCAACCAAGTGTATGCAAGCTGTGGAACGATGCAACATG 1516

QY 1276 GGATCGCTATGGGCTGCGCCCATGGAACAAGTACATCCACAGCGCTGGGTCTAGTATGG 1335

DB 1517 GGATCGCTATGGGCTGCGCCCATGGAACAAGTACATCCACAGCGCTGGGTCTAGTATGG 1576

QY 1336 CTGGCTCGCTACTCTGTGCTGCGGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1395

DB 1577 CTGGCTCGCTACTCTGTGCTGCGGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1636

QY 1396 AGGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1455

DB 1637 AGGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1696

QY 1456 TACAGAGCTGTGGTGGAGCACTGGGCTGCGGTTGAGCGAGATGCAATGCGCTGGCTGGCC 1515

DB 1697 TACAGAGCTGTGGTGGAGCACTGGGCTGCGGTTGAGCGAGATGCAATGCGCTGGCTGGCC 1756

QY 1516 GTGGACCTGTGGGCGCGCGGAGCTGAGCGCGCATGCGGCTGAGCGCTGCTGCTGCTGCTG 1575

DB 1757 GTGGACCTGTGGGCGCGCGGAGCTGAGCGCGCATGCGGCTGAGCGCTGCTGCTGCTGCTG 1816

QY 1576 CAGCGACCTGCTGCTGAGAGGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1635

DB 1817 CAGCGACCTGCTGCTGAGAGGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1876

QY 1636 GTGGCGCAGTGTGACAGATGCTGAGCTCCAGACAGTGGAGCGCGCGGCTGCTGCTGCTG 1695

QY 709 ACAGACCTGGTTCCCTGCTCTGCAATTCAGGTGTGGTGGCTAGAGCCAGACTCTGAGAGG 768
Db 977 ACAGACCTGGTTCCCTGCTCTGCAATTCAGGTGTGGTGGCTAGAGCCAGACTCTGAGAGG 1036
QY 769 GTGCAATTCCTGCCCCCTTTCCGGGAAGATCCCGGTGCAACAGGAACTCTGCGCACATAGCC 828
Db 1037 GTGCAATTCCTGCCCCCTTTCCGGGAAGATCCCGGTGCAACAGGAACTCTGCGCACATAGCC 1096
QY 829 AGGTGCGGGTACTGTCTCCAGGGGTATGCACTAGATGCGCTTGTCTGTCTGCGCGGC 888
Db 1097 AGGTGCGGGTACTGTCTCCAGGGGTATGCACTAGATGCGCTTGTCTGTCTGCGCGGC 1156
QY 889 AAGGTAACTGTGCTGGCAGGACACAGACAGAGTCCCTGCCAGCCACTTGTGCCACCA 948
Db 1157 AAGGTAACTGTGCTGGCAGGACACAGACAGAGTCCCTGCCAGCCACTTGTGCCACCA 1216
QY 949 GTGCCCCAGAAAGCCACTGTGATGAGCCACAGATTTCCAGTTTGGTGGCAGGCCAC 1008
Db 1217 GTGCCCCAGAAAGCCACTGTGATGAGCCACAGATTTCCAGTTTGGTGGCAGGCCAC 1276
QY 1009 CCCAACTCTGTGTCCAGGTGAGCACCTGGGAGAAGTTTCAGCTGCAAGGTGCTCTGTGG 1068
Db 1277 CCCAACTCTGTGTCCAGGTGAGCACCTGGGAGAAGTTTCAGCTGCAAGGTGCTCTGTGG 1336
QY 1069 GCTGACTCTTGGGGCCCTTCAAGGATGATGCTGTGTAGTGAGATGAAGAACCGGCTTC 1128
Db 1337 GCTGACTCTTGGGGCCCTTCAAGGATGATGCTGTGTAGTGAGATGAAGAACCGGCTTC 1396
QY 1129 AACAAACATCATGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1188
Db 1397 AACAAACATCATGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1456
QY 1189 TCCACGAGCTGCTGCTCCCTGGGAGGAGTTGCTGCAAGACTTCCGATCACACCACTGT 1248
Db 1457 TCCACGAGCTGCTGCTCCCTGGGAGGAGTTGCTGCAAGACTTCCGATCACACCACTGT 1516
QY 1249 ATGACGTGTGGAAACGATGACATGAGGATGCTATGGGCTTGCCTCCATGAGCAAGTAC 1308
Db 1517 ATGACGTGTGGAAACGATGACATGAGGATGCTATGGGCTTGCCTCCATGAGCAAGTAC 1576
QY 1309 ATCCACAGGCGTGGGTCTGTAGTATGCTGCGCTGCTACTCTTGTGCTGGCGCTTTTC 1368
Db 1577 ATCCACAGGCGTGGGTCTGTAGTATGCTGCGCTGCTACTCTTGTGCTGGCGCTTTTC 1636
QY 1369 TTCTTCTCTCTTAAAAAGGACCGCAGAAAGCGCCCGTGGCTCCCGCAGCGCTTG 1428
Db 1637 TTCTTCTCTCTTAAAAAGGACCGCAGAAAGCGCCCGTGGCTCCCGCAGCGCTTG 1696
QY 1429 CTCCTCACTCCCGCAGAGCGGGCTACGAGCGTCTGTGTGGAGCACTGGCGTCCGG 1488
Db 1697 CTCCTCACTCCCGCAGAGCGGGCTACGAGCGTCTGTGTGGAGCACTGGCGTCCGG 1756
QY 1489 TTGAGCCAGATGCACTGCGCGTGGCGTGGACTGTGGAGCGCGCGGAGCTGAGCGG 1548
Db 1757 TTGAGCCAGATGCACTGCGCGTGGCGTGGACTGTGGAGCGCGCGGAGCTGAGCGG 1816
QY 1549 CAGGAGCCCTAGCTGGTTCCACCAACGAGCGCGTATCTGAGGAGGTGGCGTG 1608
Db 1817 CAGGAGCCCTAGCTGGTTCCACCAACGAGCGCGTATCTGAGGAGGTGGCGTG 1876
QY 1609 GTAATCTTCTTCTTCCCGCGCGGTGGCGCAGTGTGACAGTGGCTGACGTCCAG 1668
Db 1877 GTAATCTTCTTCTTCCCGCGCGGTGGCGCAGTGTGACAGTGGCTGACGTCCAG 1936
QY 1669 ACAGTGGAGCCCGGGCGCATGACGCCCTGCGCGCTGGCTGAGTGGCTACCGAT 1728
Db 1937 ACAGTGGAGCCCGGGCGCATGACGCCCTGCGCGCTGGCTGAGTGGCTACCGAT 1996
QY 1729 TTCTTGAAGCCCGGGCGAGCCCGCTGCTAGCTGGGGTCTACTTTCAGCGGGCTGCTGAC 1788
Db 1997 TTCTTGAAGCCCGGGCGAGCCCGCTGCTAGCTGGGGTCTACTTTCAGCGGGCTGCTGAC 2056

QY 1789 CCAGACTCTGTGCTCCCGCTTCCCGTTCGCGTTCGCGCGCTTCTTCTCCCTGCCAGCAGCTG 1848
Db 2057 CCAGACTCTGTGCTCCCGCTTCCCGTTCGCGTTCGCGCGCTTCTTCTCCCTGCCAGCAGCTG 2116
QY 1849 CCGGCTTTCTCGATGCACTGCAAGGAGGCTGCTCCACTTCCGCGGGGCGACCCGCGGAC 1908
Db 2117 CCGGCTTTCTCGATGCACTGCAAGGAGGCTGCTCCACTTCCGCGGGGCGACCCGCGGAC 2176
QY 1909 CCGGTGGAAACGAGTGAACCCAGCGCTGCGGTCCGCTCGACAGCTGTACTTCTAGCTCG 1968
Db 2177 CCGGTGGAAACGAGTGAACCCAGCGCTGCGGTCCGCTCGACAGCTGTACTTCTAGCTCG 2236
QY 1969 GAAGCCCCAGGCTGCTGCGAGGAATGGACCTGGGACCCCTGCACACTACAGAA 2022
Db 2237 GAAGCCCCAGGCTGCTGCGAGGAATGGACCTGGGACCCCTGCACACTACAGAA 2290

RESULT 5
ABL34982
ID ABL34982 standard; cDNA; 2128 BP.
XX
AC ABL34982;
XX AC
XX 04-APR-2002 (first entry)
XX
DE Murine cDNA isolated from skin cells SEQ ID NO: 487.
XX
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnery;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW ss.
XX
OS Mus sp.
XX
XX WO200190357-A1.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-NZ000099.
XX
XX 24-MAY-2000; 2000US-0206650P.
XX
XX 25-JUL-2000; 2000US-0221232P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG;
PI Kumble KD;
XX
XX WPI; 2002-122020/16.
XX
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses.
XX
XX Claim 1; Page 295; 466pp; English.
XX
XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention
XX
SQ Sequence 2128 BP; 387 A; 674 C; 626 G; 441 T; 0 U; 0 Other;
Query Match 95.6%; Score 1933.6; DB 6; Length 2128;
Best Local Similarity 96.4%; Pred No. 0;
Matches 2018; Conservative 0; Mismatches 4; Indels 72; Gaps 1;

D	b	1519	ATG	C	A	G	C	T	G	G	A	A	C	G	A	T	G	A	C	A	A	T	G	G	A	T	C	G	T	A	T	G	G	C	T	G	C	C	A	T	G	C	A	A	G	T	A	C		1578		
Q	y	1309	A	T	C	A	C	A	G	G	C	G	T	G	G	T	C	T	A	G	T	A	T	G	G	T	G	C	T	A	C	T	T	G	C	T	G	C	G	C	T	T	T	C		1368						
D	b	1579	A	T	C	A	C	A	G	G	C	G	T	G	G	T	C	T	A	G	T	A	T	G	G	T	G	C	T	A	C	T	T	T	G	C	T	G	G	C	G	C	T	T	C		1638					
Q	y	1369	T	T	C	T	C	T	C	T	T	A	A	A	A	A	G	A	C	G	C	A	G	A	A	G	C	C	G	T	G	G	T	C	C	C	G	C	A	C	G	C	T	T	G		1428					
D	b	1639	T	T	C	T	C	T	C	T	T	A	A	A	A	A	A	G	A	C	G	C	A	G	A	A	G	C	C	G	T	G	G	T	C	C	C	C	A	C	G	C	T	T	G		1698					
Q	y	1429	C	T	C	T	C	A	C	T	C	G	C	C	G	A	C	G	A	G	C	G	G	T	A	C	A	G	C	G	T	T	G	T	G	G	A	G	C	A	T	G	C	G	T	C	G		1488			
D	b	1699	C	T	C	T	C	A	C	T	C	G	C	G	A	C	G	A	G	C	G	G	T	A	C	A	G	C	G	T	A	C	T	T	G	G	A	G	C	A	T	G	C	G	T	C	G		1758			
Q	y	1489	T	T	G	A	G	C	A	G	A	T	G	C	A	C	T	G	C	G	T	G	C	T	G	G	A	C	T	G	T	G	G	A	C	C	C	C	G	A	G	C	T	G	A	C	G		1548			
D	b	1759	T	T	G	A	G	C	A	G	A	T	G	C	A	C	T	G	C	G	T	G	C	T	G	G	A	C	T	G	T	G	G	A	C	C	C	C	G	A	G	C	T	G	A	C	G		1818			
Q	y	1549	C	A	C	G	A	G	C	C	T	A	G	C	T	G	T	T	C	C	A	C	A	C	A	C	A	G	C	G	C	T	A	C	C	A	C	G	C	C	T	A	C	T	G	A	C	G		1608		
D	b	1819	C	A	C	G	A	G	C	C	T	A	G	C	T	G	T	T	C	C	A	C	A	C	A	C	A	G	C	G	C	T	A	C	C	A	C	G	A	C	C	T	A	C	T	G	A	C	G		1878	
Q	y	1609	G	T	A	T	C	C	T	T	C	T	C	C	C	C	G	C	G	C	G	T	G	C	G	A	G	T	G	T	C	A	G	A	G	T	G	T	G	C	G	T	A	C	C	G		1668				
D	b	1879	G	T	A	T	C	C	T	T	C	T	C	C	C	C	G	C	G	C	G	T	G	C	G	A	G	T	G	T	C	A	G	A	G	T	G	T	G	C	A	G	T	C	C	A		1938				
Q	y	1669	A	C	A	G	T	G	A	G	C	C	G	C	C	G	A	T	A	G	C	C	C	T	G	C	C	C	T	G	C	G	C	T	G	C	T	C	A	G	T	G	C	T	A	C	C	C	G	A		1728
D	b	1939	A	C	A	G	T	G	A	G	C	C	G	C	C	G	A	T	A	G	C	C	C	T	G	C	C	C	T	G	C	C	C	C	T	G	C	T	A	G	T	G	C	T	A	C	C	C	G	A		1998
Q	y	1729	T	T	C	T	G	C	A	A	G	C	C	G	C	G	C	G	A	C	C	G	C	G	C	T	A	G	T	C	G	C	G</																			

RESULT 7	
AEB5651	
ID AEB5651 standard; cDNA; 2314 BP.	
XX	
AC AEB5651;	
XX	
DT 22-SEP-2005 (first entry)	
XX	
DE Mouse DCSR7 polypeptide encoding cDNA.	
XX	
KW protein engineering; cytokine receptor; DNAX cytokine receptor subunit;	
KW DCSR; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;	
KW interstitial lung disorder; asthma; allergy; atherosclerosis;	
KW gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;	
KW gastropneumatic; antiatherosclerotic; respiratory-gen.; immunosuppressive;	
KW antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;	
KW IL-17C agonist; mouse; DCSR7; gene; ss; antisense therapy; RNAi therapy.	
XX	
OS Mus musculus.	
XX	
Key Key	Location/Qualifiers
FH .FT CDS	199..2295

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FT	/product= "DCRS7"	
FT	199. .2292	
FT	/*tag= b	
FT	199. .258	
FT	/*tag= a	
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XX	WO2005065711-A2.	
PN		
XX		
PD	21-JUL-2005.	
XX		
XX	22-DEC-2004; 2004WO-US042935.	
PF		
XX		
XX	29-DEC-2003; 2003US-00749144.	
PR		
XX		
PA	(SCHE) SCHERING CORP.	
XX		
XX	Gorman DM;	
PI		
XX		
XX	WPI; 2005-506792/51.	
DR	P-PSDB; AER55652.	
DR		
XX		
PT	Modulating activity of cell, involves contacting cell with an agonist or	
PT	antagonist of DNAX cytokine receptor subunit.	
XX		
XX	Example 5; SEQ ID NO 7; 130pp; English.	
PS		
XX		
CC	The invention relates to modulating (M1) activity of cell, by contacting	
CC	cell with an agonist or antagonist of DNAX cytokine receptor subunit	
CC	(DCRS9) or of interleukin (IL)-17C where the cell modulates psoriasis,	
CC	inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or	
CC	allergy, or atherosclerosis. Also provided are methods for treating (M2)	
CC	the disorders which involves administration of the modulator and	
CC	diagnosing (M3) a disorder as mentioned above that involves contacting a	
CC	sample from a test subject with a binding composition that specifically	
CC	binds to a polypeptide or nucleic acid of DCRS9 or IL-17C. (M1) is useful	
CC	for modulating an activity of a cell. (M2) is useful for treating a	
CC	subject suffering from a disorder such as psoriasis, IBD, interstitial	
CC	lung disorder, asthma or allergy, or atherosclerosis, where the	
CC	interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic	
CC	granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or	
CC	ulcerative colitis. The present sequence represents a mouse DCRS7	
CC	polypeptide encoding cdNA.	
XX		

	Query Match	95.6%;	Score 1933..6;	DB 14;	Length 2314;
	Best Local Similarity	96.4%;	Pred. No. 0;		
	Matches 2018;	Conservative	0;	Mismatches	4;
				Indels	72;
				Gaps	1;
QY	1	ATGCCTGTGTCCTGGTTCCTCTCTCTGTCTGTGGCACTGGCCGAAACCTGTGGTCTCTCT	60		
Db	199	ATGCCTGTGTCCTGGTTCCTCTCTGTGGCACTGGCCGAAACCTGTGGTCTCTCTCT	258		
QY	61	CTGGAGACACTGATGGAGCCTCAGACACTCAGCGTCTCTCTAGGCCTCTCTTCGCCAC	120		
Db	259	CTGGAGACACTGATGGAGCCTCAGACACTGCA CGCTCTCTCTAGGCCTCTCTTCGCCAC	318		
QY	121	CTCTGGGATGTGTGACGTGCTCTGCTGTGCTGGAGCCTCCAGTCTGCCCGAGGCCCTGTG	180		
Db	319	CTCTGGATGTGTGACGTGCTCTGCTGTGCTGGAGCCTCCAGTCTGCCCGAGGCCCTGTG	378		
QY	181	CTAGTGCCCTACCCGCTTCAGACGAGCTGGTGCTGAGGTGTCCA CAGAAGACAGATTGC	240		
Db	379	CTAGTGCCCTACCCGCTTCAGACGAGCTGGTGCTGAGGTGTCCA CAGAAGACAGATTGC	438		
QY	241	GCCCTCCGTGTCCGTGTGTGTGTCCACTTGTGGCCGTGCTATGGGCATCTGGGCAGAGCTGAA	300		
Db	439	GCCCTCTGTGTCCGTGTGTGTGTCCACTTGTGGCCGTGCTATGGGCATCTGGGCAGAGCTGAA	498		
QY	301	GAAGCTGGAAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAA GCGCTCTCTCCAGGCCCCAG	360		
Db	499	GAAGCTGGAAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAA GCGCTCTCTCCAGGCCCCAG	558		

Qy	361	GTGGTGTCTCTCTCTTCAGAGCCTACCCCATCGCCCGCTGTGTGCCCTGTCTGGAGGTCCAGGTG	420
Db	559	GTGGTGTCTCTCTCTTCAGAGCCTACCCCATCGCCCGCTGTGTGCCCTGTCTGGAGGTCCAGGTG	618
Qy	421	CCCGCTGACCTGTGTGCGACCTGTGTGCTGCTGCGGTCTGTGGGTATTTGACTGTGTTTCGAG	480
Db	619	CCCGCTGACCTGTGTGCGACCTGTGTGCTGCTGCGGTCTGTGGGTATTTGACTGTGTTTCGAG	678
Qy	481	GCTAGTCTTTGGGGCTGAGGTACAGATCTGTGCTTACACGAAGCCCAAGTACACAGAAAGAG	540
Db	679	GCTAGTCTTTGGGGCTGAGGTACAGATCTGTGCTTACACGAAGCCCAAGTACACAGAAAGAG	738
Qy	541	CTCAACCTTCAACAGCAGCTGCCT-----	564
Db	739	CTCAACCTTCAACAGCAGCTGCCTGTGACGGGGTCTTGAAGTCCCGGACAGCATCCAG	798
Qy	565	-----GATGGTGAATATGCTTCTTGACAC	588
Db	799	AGTGTGTGGGTCTGTGCCCTGGCTCAATGTGTCTACAGATGTGTGACAAATGTCTTCTGACA	858
Qy	589	CTGATATGTCTCTGAGGAGCAGGACTTTTAGTCTTTACTGTACTGTGCGTTCAGTCCCGCGAT	648
Db	859	CTGATATGTCTCTGAGGAGCAGGACTTTTAGTCTTTACTGTACTGTGCGTTCAGTCCCGCGAT	918
Qy	649	GCTCTCAAAATCTTTGTGGTACAAAACCTGTACTGGACCTCAGAACTATTTACTTTAAACCCAC	708
Db	919	GCTCTCAAAATCTTTGTGGTACAAAACCTGTACTGGACCTCAGAACTATTTACTTTAAACCCAC	978
Qy	709	ACAGACCTGTGTTCCCTGTCTGCAATTCAGGTGTGTGTCTAGAGCCAGACTCTGAGAGG	768
Db	979	ACAGACCTGTGTTCCCTGTCTGCAATTCAGGTGTGTGTCTAGAGCCAGACTCTGAGAGG	1038
Qy	769	GTGGAAATCTGCCCCCTTCGCGGAAGATCCCGGTGCACACAGGAACCTCTGSCACATAGCC	828
Db	1039	GTGGAAATCTGCCCCCTTCGCGGAAGATCCCGGTGCACACAGGAACCTCTGSCACATAGCC	1098
Qy	829	AGGCTGTGGGTACTGTCTCCAGGGGTATGGCAGCTAGATGCGCTTGTCTGTCTGCGCGGGC	888
Db	1099	AGGCTGTGGGTACTGTCTCCAGGGGTATGGCAGCTAGATGCGCTTGTCTGTCTGCGCGGGC	1158
Qy	889	AAGGTAACTGTGTCTGGCAGGCACACAGACAGAGTCCCTGCCAGCCACTTGTGTGCCACCA	948
Db	1159	AAGGTAACTGTGTCTGGCAGGCACACAGACAGAGTCCCTGCCAGCCACTTGTGTGCCACCA	1218
Qy	949	GTCCCCCAGAGAACGCCACTGTGAAATGAGCCCAACAGATTTCCAGTTTGGTGGCAGGCCAC	1008
Db	1219	GTCCCCCAGAGAACGCCACTGTGAAATGAGCCCAACAGATTTCCAGTTTGGTGGCAGGCCAC	1278
Qy	1009	CCCAACTCTGTGTCTGAGTGTGAGCACCTGGGAGAGGTTCAGCTGTCAAGCGTGTCTGTGTGG	1068
Db	1279	CCCAACTCTGTGTCTGAGTGTGAGCACCTGGGAGAGGTTCAGCTGTCAAGCGTGTCTGTGTGG	1338
Qy	1069	GCTGACTCTTTGGGGCCCTTCAAGGATGATACTGTGTAGTGGAGATGAAAAACCGGCTTC	1128
Db	1339	GCTGACTCTTTGGGGCCCTTCAAGGATGATACTGTGTAGTGGAGATGAAAAACCGGCTTC	1398
Qy	1129	AACAAACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTGTACCACTGCCAGGATGGCC	1188
Db	1399	AACAAACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTGTACCACTGCCAGGATGGCC	1458
Qy	1189	TCCACAGAGAGTGTCTGCCCTGGGAGAGGAGTGTGTCAAGACTTCCGATCACACCCAGTGT	1248
Db	1459	TCCACAGAGAGTGTCTGCCCTGGGAGAGGAGTGTGTCAAGACTTCCGATCACACCCAGTGT	1518
Qy	1249	ATGCAGCTGTGGAACGATGACAAATGTGGATTCGCTATGGGCTGTGCCCATGTGACAGTAC	1308
Db	1519	ATGCAGCTGTGGAACGATGACAAATGTGGATTCGCTATGGGCTGTGCCCATGTGACAGTAC	1578
Qy	1309	ATCCAAGGCGCTGGGTCTTAGTATGCTGTGGCTGTGGCTGTCTTGTGGCTGTGGGCGCTTTTC	1368
Db	1579	ATCCAAGGCGCTGGGTCTTAGTATGCTGTGGCTGTGGCTGTCTTGTGGCTGTGGGCGCTTTTC	1638

QY	1369	TTCCTTCCCTCCTTTAAAAAAAGGACCGCAGGAAGCGGCCGTGGCTCCCCGCACGCGCCCTTG	1428
Db	1639	TTCTTCCCTCCTTTCTAAAAGGACCGCAGGAAGCGGCCGTGGCTCCCCGCACGCGCCCTTG	1698
QY	1429	CTCCTCCCACTCCGCGCAGGAGCGGGCTACGAGCGTCTGCTGGAGACACTGGCGTCCGCG	1488
Db	1699	CTCCTCCAATCCGCGCAGGAGCGGGCTACGAGCGCTGCTGGAGACACTGGCGTCCGCG	1758
QY	1489	TTGAGCCAGATGCCACTCTCGCGTGGCCCTGGACCTGTGGAGCGCCGCCGACGCTGAGCGCG	1548
Db	1759	TTGAGCCAGATGCCACTCTCGCGTGGCCCTGGACCTGTGGAGCGCCGCCGACGCTGAGCGCG	1818
QY	1549	CACGGAGCCCTAGCTGGTTCACACCACGACGACCGCGTATCTCTGCAGGAGGTGGCGTG	1608
Db	1819	CACGGAGCCCTAGCTGGTTCACACCACGACGACCGCGTATCTCTGCAGGAGGTGGCGTG	1878
QY	1609	GTAATCCTTCTCTTCGCGCGGGCCGTGGCGCAGTGTCTCAGCAGTGGCTGCGAGCTCCAG	1668
Db	1879	GTAATCCTTCTCTTCGCGCGGGCCGTGGCGCAGTGTCTCAGCAGTGGCTGCGAGCTCCAG	1938
QY	1669	ACAGTAGAGCCCGGGCCGATGACGCCCTCGCCGCTGGCTCAGCTGCGTGTACCCGAT	1728
Db	1939	ACAGTAGAGCCCGGGCCGATGACGCCCTCGCCGCTGGCTCAGCTGCGTGTACCCGAT	1998
QY	1729	TTCTCGAAGCCGGGCGACCGCGCTACGTGCGGGTCTATTTCGACGGGCTGCTGCAC	1788
Db	1999	TTCTCGAAGCCGGGCGACCGCGCTACGTGCGGGTCTATTTCGACGGGCTGCTGCAC	2058
QY	1789	CCAGACTCTGTGCGCTCCCGCTTCGCGGTGCGCCGCTCTTCTCTCCGCCACGCGAGCTG	1848
Db	2059	CCAGACTCTGTGCGCTCCCGCTTCGCGGTGCGCCGCTCTTCTCTCCGCCCTGCGAGCTG	2118
QY	1849	CCGGCTTTCTTGATGACACTCGAGGAGGCTGCTCCACTTCGCGGGGCGACCCCGGGAC	1908
Db	2119	CCGGCTTTCTTGATGACACTCGAGGAGGCTGCTCCACTTCGCGGGGCGACCCCGGGAC	2178
QY	1909	CGGCTGGAACGAGTGACCCAGGCGCTGCGGTCCGCCCTTGGACAGCTGTACTTCTAGCTCG	1968
Db	2179	CGGCTGGAACGAGTGACCCAGGCGCTGCGGTCCGCCCTTGGACAGCTGTACTTCTAGCTCG	2238
QY	1969	GAAGCCCAGGCTGCTCGGAGGAAATGGGACCTGGGACCTGCACTACCTAGAA	2022
Db	2239	GAAGCCCAGGCTGCTCGGAGGAAATGGGACCTGGGACCTGCACTACCTAGAA	2292
RESULT 8			
ABK86568			
ID	ABK86568 standard; cDNA; 2331 BP.		
XX			
AC	ABK86568;		
XX			
DT	24-SEP-2002 (first entry)		
XX			
DE	Mouse interleukin 17 receptor like protein, IL-17RL, full length cDNA.		
XX			
KW	Mouse; ss; gene; Interleukin 17 receptor-like protein; IL-17RL;		
KW	chondrolectin; bone degradation; cartilage degradation; gene therapy;		
KW	chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;		
KW	allergic skin immune response; organ transplant rejection; cycokine;		
KW	osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;		
XX	seronegative spondyloathropathy; bone morphogenetic protein.		
OS	Mus sp.		
XX			
FH	Key Location/Qualifiers		
FT	199..2295		
CDS	/*tag= a		
FT	/*product= "IL-17RL"		
FT	/*transl_except= (pos:2077..2079,aa:Xaa)		
FT	/*transl_except= (pos:2161..2163,aa:Xaa)		
FT	/*transl_except= (pos:2200..2202,aa:Xaa)		
FT	/*transl_except= (pos:2242..2244,aa:Xaa)		
FT	/*note= "Xaa is unknown"		

W0200238764-A2.

16-MAY-2002.

13-NOV-2001; 2001WO-US043855.

10-NOV-2000; 2000US-0247134P.
23-FEB-2001; 2001US-0271197P.
12-OCT-2001; 2001US-0328904P.

(REGC) UNIV CALIFORNIA.

Haudenschild D, Rose L, Moseley T, Reddi AH;
WPI; 2002-508211/54.
P-PSTD; AAU99161.

Interleukin-17 receptor-like polypeptide useful for the manufacture of a medicament to modulate cartilage or bone growth in a mammal.

Claim 84; Page 88-89; 108pp; English.

The invention relates to an interleukin-17 receptor-like (IL-17RL) polypeptide, with 85% or greater sequence identity to a polypeptide with a sequence appearing as AAU98781-AAU98792, where IL-17RL binds to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F. Also included are IL-17RL polynucleotides, antibodies, expression cassettes, transgenic host cells, a method of determining the presence or absence in the cell of a cancer cell, by determining the presence or absence in the cell of a group of IL-17RL (where the determination that the group is absent in the cell indicates that the cancer is more aggressive than a like cell in which the group is present) and a mammalian cell comprising a polynucleotide encoding an IL-17B antagonist, where the cell is selected from chondrocyte, synovocyte, and mesenchymal stem cell. IL-17RL or the polynucleotide is useful for the manufacture of a medicament to modulate cartilage or bone growth in a mammal. The polynucleotide is useful for the manufacture of a medicament to restore androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL is useful for inhibiting ossification or calcification in a mammal suffering from pathological disorder in a mammal, for diagnosing a cartilage degenerative disease in a mammal, for inhibiting the rate of proteoglycan synthesis by a chondrocyte in culture, and for the manufacture of a medicament to potentiate the activity of a bone morphogenetic protein in a mammal. An IL-17RL antagonist is useful for treating a bone or cartilage pathology such as a degenerative cartilage disorder selected from osteoarthritis, rheumatoid arthritis, relapsing polycondritis, allergic skin immune response spondyloarthropathies, multiple sclerosis, and organ transplant rejection. IL-17RL is particularly a receptor for IL-17B (chondroleukin, a proinflammatory cytokine). The gene for IL-17RL is located on chromosome 3p25.3-3p24.1. The present sequence is the full length cDNA sequence for mouse IL-17RL

Sequence 2331 BP; 428 A; 725 C; 695 G; 473 T; 0 U; 10 Other;

Query Match 95.4%; Score 1929.6; DB 6; Length 2331;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 2011; Conservative 6; Mismatches 5; Indels 72; Gaps 1;

QY 1 ATGCTGTGTCCTGGTTTCTGCTGCTCTTGCGACATGGCCGGAACCCTGTGGTGCCTCT 60
DB |||||
 199 ATGCCGTGTCTCTGGTTCTGCTCTCTGCGACTGGCGCAACCCCTGTGGTGCCTCT 258
QY 61 CTGAGAGACATGATGAGCCTCAGAACACTGCAGCTGCTCTTAGGCCCTCTCTGCCAC 120
DB |||||
 259 CTGAGAGACATGATGAGCCTCAGAACACTGCAGCTGCTCTTAGGCCCTCTCTGCCAC 318
QY 121 CTCCTGGATGGTACGTCTCTGCTGCTGCTGCTGAAAGCTCCAATGCTGCCGCCCTGTG 180
DB |||||
 319 CTCCTGGATGGTACGTCTCTGCTGCTGCTGCTGAAAGCTCCAATGCTGCCGCCCTGTG 378
QY 181 CTGATGCTTACCCGCTCAGACGAGGCTGGTGTGAGGTGCTCCACAGAACAAGATTGC 240

Db 1459 TCACGAGAGCTGCTGCGCTGGGAGAGAGTTGCTGCAAGACTTCGATCACACAGTGT 1518
Qy 1249 ATGAGCTGTGGAAAGCATGACATGATGGATCGCTATGGGCTGCGCCCATGGACAAGTAC 1308
Db 1519 ATGAGCTGTGGAAAGCATGACATGATGGATCGCTATGGGCTGCGCCCATGGACAAGTAC 1578
Qy 1309 ATCCACAGGCGCTGGTCTTAGTATGGCTGGCTGCTACTCTTGGCTGGGGCTTTTC 1368
Db 1579 ATCCACAGGCGCTGGTCTTAGTATGGCTGGCTGCTACTCTTGGCTGGGGCTTTTC 1638
Qy 1369 TTCTTCTCTCTTCTAATAAAGGACCGCAGGAAGCGCGCTGGCTCCCGCAGCGCTTG 1428
Db 1639 TTCTTCTCTCTTCTAATAAAGGACCGCAGGAAGCGCGCTGGCTCCCGCAGCGCTTG 1698
Qy 1429 CTCTCCACTCCGCGCAGCGGCTACGAGCGTCTGATGGAGCACTGGCGTCCGCG 1488
Db 1699 CTCTCCACTCCGCGCAGCGGCTACGAGCGTCTGATGGAGCACTGGCGTCCGCG 1758
Qy 1489 TTGAGCCAGATGCACTGGCGCTGGCGCTGGGACCTGTGGAGCGCGCGAGCTGAGCGG 1548
Db 1759 TTGAGCCAGATGCACTGGCGCTGGCGCTGGGACCTGTGGAGCGCGCGAGCTGAGCGG 1818
Qy 1549 CAGGAGCCCTAGCTGTGTTCCACCAACGAGCGCGCTATCTGAGAGAGGCTGCGG 1608
Db 1819 CAGGAGCCCTAGCTGTGTTCCACCAACGAGCGCGCTATCTGAGAGAGGCTGCGG 1878
Qy 1609 GTAATCCTTCTCTTCTGCGCGCGCGCTGCGCAGTGTGAGTGGCTGAGCTCCAG 1668
Db 1879 GTAATCCTTCTCTTCTGCGCGCGCGCTGCGCAGTGTGAGTGGCTGAGCTCCAG 1938
Qy 1669 ACAGTGGAGCCGCGCGCATGACGCTGCGCGCTGCTGAGTGTGCTTACCCGAT 1728
Db 1939 ACAGTGGAGCCGCGCGCATGACGCTGCGCGCTGCTGAGTGTGCTTACCCGAT 1998
Qy 1729 TTCTCTCAAGGCGGCGGACCGCGCTGCTGCGGCTCTTCTGACAGGCTGCTGCAC 1788
Db 1999 TTCTCTCAAGGCGGCGGACCGCGCTGCTGCGGCTCTTCTGACAGGCTGCTGCAC 2058
Qy 1789 CCAGACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1848
Db 2059 CCAGACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2118
Qy 1849 CCGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1908
Db 2119 CCGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2178
Qy 1909 CCGGTGGACGAGTGACCCAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1968
Db 2179 CCGGTGGACGAGTGACCCAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 2238
Qy 1969 GAAGCCCCAGGCTGCTGCGAGGAATGGGACCTGGGACCTGGGACCTGGGACCTAGAA 2022
Db 2239 GAASCCCCAGGCTGCTGCGAGGAATGGGACCTGGGACCTGGGACCTGGGACCTAGAA 2292

RESULT 9
ID AAD24221
XX AAD24221 standard; DNA; 2022 BP.
AC AAD24221;
XX AAD24221;
XX 17-MAY-2002 (first entry)
DT Murine cytokine receptor, Zcytor14 degenerate DNA.
DE Murine; cytokine receptor, Zcytor14, inflammation; rheumatoid arthritis;
XX Gene therapy; protein therapy; ds.
KW Mus sp.
XX WO200204519-A2.
PN 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US021344.
XX 06-JUL-2000; 2000US-021646P.
XX (ZYMO) ZYMOGENETICS INC.
PA Gao Z;
PI WPI; 2002-179701/23.
DR New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
XX receptor, useful for treating inflammation, specifically rheumatoid
XX arthritis, and as educational tools or in research.
XX Claim 8; Page 92; 99pp; English.
XX The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
XX polypeptide is useful for identifying or isolating Zcytor14 ligands, in
XX preparing antibodies, in identifying proteins or peptide cleavage sites,
XX in amino acid sequence analysis, and in monitoring biological activities
XX of both the native and tagged protein in vitro or in vivo. Polypeptides
XX having Zcytor14 activity can be used to treat inflammation, such as
XX rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational
XX tool in genetics, molecular biology, protein chemistry and antibody
XX production analysis, in the preparation of expression constructs for
XX bacterial, viral or mammalian expression, in determining mRNA and DNA
XX localisation of Zcytor14 polynucleotide in tissues, for identifying
XX related polynucleotides and polypeptides by nucleic acid hybridisation,
XX in linkage-based testing for various diseases in murine models, and to
XX determine whether a subject's chromosomes contain a mutation in the
XX Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo
XX diagnosis, and for detecting and localising Zcytor14 gene expression in
XX tissue samples. The present sequence is a degenerate form of DNA encoding
XX murine cytokine receptor, Zcytor14 (AAB14559)
SQ Sequence 2022 BP; 240 A; 248 C; 377 G; 272 T; 0 U; 885 Other;
Query Match 69.8%; Score 1412.2; DB 6; Length 2022;
Best Local Similarity 56.2%; Pred. No. 1.6e-301;
Matches 1137; Conservative 464; Mismatches 421; Indels 0; Gaps 0;
Qy 1 ATGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 ATGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy 61 CTGGAGACTGATGGAGCGCTCAGGACACTGACGCTCTCTCTAGGCTCTCTCTGCTGCT 120
Db 61 YTGARMGNTYATGGARCCNCARGAYACNGCNMGNTGYNSYNTGNGNTYNSNTGYCAY 120
Qy 121 CTCTGGGATGTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 YNTGGGAYGNGAYGTNTYNTGTYTNCNGNWSNTYTCARWSNGCNCNGCNGCNGTN 180
Qy 181 CTAGTGCTTACCCGCTCAGCAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 YTGNTCCNACNMGNNTYTCARACNGARYTNGTNTYNTMGNTGYCCNCARABACNGAYTG 240
Qy 241 GCGCTCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 GNTYNTMGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 300
Qy 301 GAAGCTGGAAGTCTGATTAGAACTCCAGGAGCTTAGGAAAGCGCTCTCTCTCAGGCCAG 360
Db 301 GARGCNGNARWSNGAYWSNGARYTNCARGARWSNMGNAYGCMWSNTYTCARGCNCAR 360
Qy 361 GTGCTGCTCTCTTCCAGGCTTACCCCATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 GTNGTNTYNTGNTYTCARGCNTAYCCNATGNCNMGNTGYCNCYNTYNTGARGTNCARGTN 420
Qy 421 CCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 CCNGCNGAYTNTGNTNCARCCNGCNGNARWSNGTNGNWSNGCNGTNTTGYATGYTGYAR 480

QY	481	GCTAGCTTTGGGCTGAGTACAGATCTGTGCTCTACACAGAGCCAGGTACACAGAAAGAG	540	1561	GCTGTCTTCCACACACAGCAGCGGTATCTCTGAGGAGGGTGGCGTGGTATCTCTTC	1620
Db	481	GCNWSNYTNGGNCNGARGTNCARATHGGHNSNTAYACNAARCCNMGNATYCARAARGAR	540	1561	GCNTGGTTTCAYCAYCARMNGNMGNAHYTNCARGAGGNGGNGTNGTNTATHTYNTYN	1620
QY	541	CTCAACCTCACACAGACGCTGCCTGATGGTGACAAATGCTCTCTGACACTGGATGCTCT	600	1621	TTCTCCGCCCGCGCGGTGGCGAGTGTGACAGTGGCTGACAGTCCAGACAGTGGAGCC	1680
Db	541	YTNAAVYTNACNARCARYTNCNGAYGGNGAYAAAGTNTYNTNACNYTNGAYGTWNS	600	1621	TTVWSNCCNGCNGCNGTNGCNCARTGYCARCARTGGYTNCARTYTNARACNGTNGARCN	1680
QY	601	GAGGAGCAGGACTTAGCTCTTACTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660	1681	GGGCGCCATGAGCCTCGCCCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
Db	601	GARGARCARGATTTTWSNTTYTNTAYTNTGNCNGCNGCNGCNGCNGCNGCNGCNGCNG	660	1681	GNCCNCAVAYGCTYNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG	1740
QY	661	TTGTGCTCAAAAACCTGACTGGAACCTCAGAACATTAATCTTTAAACCAACAGACTGCT	720	1741	CGGCGCACCGCGCGCTACGTGCGGGGTCTACTTCCGAGCGGCTGCTGACCCGACTCTG	1800
Db	661	YNTGTGTAARAAVYTNACNGCNCARAAVATHACNYTNAAYCAVACNGAYTNGTN	720	1741	MGNCCNACNGNMGNTAYTNGGNGTNTAYTYGAYGNYTNTYTCAYCNGAYNSNGTN	1800
QY	721	CCCTGCTCTGATTCAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780	1801	CCCTCCCGCTTCCGCTGCGCGCTCTTCTTCCCTGCGCACGAGCTGCGGGCTTTCCTG	1860
Db	721	CCNTGYTNTGATHCARGTNTGWSNTYNGARCNGCNGAYWSNGARMGNGTNGARTTYG	780	1801	CCNWSNCCNTYTMGNGTNGCNCNTYNTTYSNYTNCNACNARYTNCNGCNYTNTYTN	1860
QY	781	CCCTTCCGGAAGATCCCGGTGCACACAGAACTCTGGCACATAGCCAGGCTGCGGGTA	840	1861	GATGCACTGACGAGGAGCTGCTCCACTTCGCGGGGCGACCCCGGACCGGGTGGAAACGA	1920
Db	781	CCNTTVMNGARAGAYCCNGGNGCNCAYMGNAAVYNTGCAVATHGCMNGNYTMNGNTN	840	1861	GAYCCTTNCARGNGGNTGYWSNACNWSNGCNGNMGNCNGCNGAYMGNGTNGARMGN	1920
QY	841	CTGTCCCGAGGGTATGCGAGCTAGATGCGCTTGTCTGCTGCGGGCAGGTAACACTG	900	1921	GTGACCCAGCGCTGCGGCTCCGCTGCGACAGCTGTACTTCTAGCTCGGAAGCCCGAGC	1980
Db	841	YTNWSNCCNGGNTTGGCARYTNGAYCNCNTGYTYTNCNGNAAAGTNAACNTYN	900	1921	GTNACNARGCNYTMNGNWSNGCNYTNGAYWSNTGYACNWSNWSNWSNGARCCNCGN	1980
QY	901	TGCTGGAGGCCACACAGACAGTCCCTGCGAGCACCTTGTGCGCACAGTGGCCAGAG	960	1981	TGCTGCGAGGAATGGGACCTGGGACCTGGCACTACACTAGAA	2022
Db	901	TGYTGGCARGCNCNGAYCARNSNCCNTGYCARCNGTNTGNCNCCNGTNCNCABAR	960	1981	TGYTGYGARGARTGGGAYTNGGNCNTGYACNACNYTNGAR	2022
QY	961	AACGCCACTGTGAATGAGCCACAGATTTCCAGTTGGTGGCAGGCGACCCCAACCTCTGT	1020	RESULT 10		
Db	961	AATGNCNCTNAAVYGNARCCNARGATYTCARYTNGTNGCNGCNGCAYCCNAAVYNTGY	1020	AAD24223 standard; DNA; 2094 BP.		
QY	1021	GTCCAGTGTGACCTGGGAGAGGTTACGCTCAAGCGTGTCTGCGGGCTGACTCTCTTG	1080	XX AAD24223;		
Db	1021	GTNCARGTNSNACNTGGGARAARGTNCARYTNCARGCMTGYWSNTGGGCGGAYNSNTN	1080	XX 17-MAY-2002 (first entry)		
QY	1081	GGGCTCTCAAGATGATGCTGTAGTGGAGATGAACACCGGCTCAACACACATCA	1140	DE Murine Zcytor14 cytokine receptor variant, Zcytor14-1 degenerate DNA.		
Db	1081	GGNCNTTYAARGAYATGYNTYNTGNGARATGAARACNGNYTNAAYAAVACNWSN	1140	XX Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;		
QY	1141	GTCTGTGCTTGGAAACCACTGGCTGTAACCACTGCGCCAGCATGGCTCCAGAGCT	1200	XX gene therapy; protein therapy; Zcytor14-1; ds.		
Db	1141	GTNTGYCNYTNGARCCNWSNGNTGYACNCCNYTNCNWSNATGGCNCNWSNACNMGNCN	1200	XX Mus sp.		
QY	1201	GCTCGCTGGGAGAGGATGCTGCAAGACTTCCGATCACACAGTGTATGCAAGCTGTG	1260	XX WO200204519-A2.		
Db	1201	GCNNGTNGGNGARGARYTNTYTCARGAYTNGGNGCNGCNGCNGCNGCNGCNGCNGCNG	1260	XX 17-JAN-2002.		
QY	1261	AACGATGACAACTGGATCGCTATGGGCTGCGCCATGGAAGTACATCCACAGCGC	1320	XX 05-JUL-2001; 2001WO-US021344.		
Db	1261	AAAGAYGAYATGGGWSNYTNGGCTGCGATGCGATGAYAAATAYATHCAVGMNGN	1320	XX 06-JUL-2000; 2000US-0216446P.		
QY	1321	TGGGTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380	XX (ZYMO) ZYMOGENETICS INC.		
Db	1321	TGGGTNTGNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380	XX Gao Z;		
QY	1381	CTAAAAGGACCCGAGGAGGCTGCTGCAAGCTTCCGATCACACAGTGTATGCAAGCTGTG	1440	XX WPI; 2002-179701/23.		
Db	1381	YTNAAARGAYMGNMGAARCGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG	1440	XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the		
QY	1441	GCNGAYGGCNGGNTAYGARMGNTNGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG	1500	XX receptor, useful for treating inflammation, specifically rheumatoid		
Db	1441	GCNGAYGGCNGGNTAYGARMGNTNGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG	1500	XX arthritis, and as educational tools or in research.		
QY	1501	CACTGCGGCTGGCTGAGTGTGGAGCGCCGCGAGCTGAGCGCGCAGCGAGCCCTA	1560	XX Claim 8; Page 97-98; 99pp; English.		
Db	1501	CCNYTMNGTNGCNGTNGAYTNTGGWSNMGNMGNMGNMGNMGNMGNMGNMGNMGNMGN	1560	XX The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14		
				XX polypeptide is useful for identifying or isolating Zcytor14 ligands, in		
				XX preparing antibodies, in identifying proteins or peptide cleavage sites,		
				XX in amino acid sequence analysis, and in monitoring biological activities		
				XX of both the native and tagged protein in vitro or in vivo. Polypeptides		

having Zcytor14 activity can be used to treat inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational tool in genetics, molecular biology, protein chemistry and antibody production analysis, in the preparation of expression constructs for bacterial, viral or mammalian expression, in determining mRNA and DNA localisation of Zcytor14 polynucleotide in tissues, for identifying related polynucleotides and polypeptides by nucleic acid hybridisation, in linkage-based testing for various diseases in murine models, and to determine whether a subject's chromosomes contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for *in vivo* diagnosis, and for detecting and localising Zcytor14 gene expression in tissue samples. The present sequence is a degenerate form of DNA encoding murine Zcytor14 variant, Zcytor14-1 (AAE14560)

Sequence 2094 BP: 248 A; 252 C; 393 G; 283 T; 0 U; 918 Other:

Query Match	65.8%	Score 1330.2;	DB 6;	Length 2094;
Best Local Similarity	54.3%	Pred. NO. 2e-283;		
Matches 1137; Conservative	464;	Mismatches 421;	Indels 72;	Gaps 14

[illegible]

Db	781	ACNGAYTNGTNCNTGYTNTGYATHCARGTNTGWSNNTNGARCNNGAYWSNGARMGN	840
Qy	769	GTCCAAATTCCTGCCCTTCCTCGGGAGATCCCGGTGGCAACACAGGAACCTCTGGCACATAGCC	828
Db	841	GTNGARTTYTGYCNTTYTNGNGARGAYCCNGGNGCNAYMGNAAAYTNTTGGCAYATHGNC	900
Qy	829	AGGCTGGGGTACTGTCTCCACAGGGGTATGCAGCTAGATGCGCTTGCTGTCTGCGCGGGC	888
Db	901	MENYTNMGNGTNTYTNWSCNCGNGNGTNTGGCARYTNGAYGCNCCNTGYTYTNTCCNGGN	960
Qy	889	AAGGTAACTATGTGCTGGCAGGCAACAGACAGAGTCCCTGCGAGCACTTGTGGCAACCA	948
Db	961	AARTNACNTNTGYTGGCARGCNCNGAYCARWSNCCNTGYCARCENYTNGTNCCNCCN	1020
Qy	949	GTGCCCCAGAGAACGCCACTGTGTAATGAGCCACCAAGATTTCCAGTGTGGTGAGGCCAC	1008
Db	1021	GTNCCNCAARAAYGCNACNTGNTAAAYGARCCNCARGAYTTYCARYTNGTNGCNGNCAY	1080
Qy	1009	CCCAAACCTCTGTCTCAGGTGAGCACTGGGAGAAAGTTCAGCTGCAAGCGTCTCGTGG	1068
Db	1081	CCNAAYYTNTGYTNCARGTNWSNACNTGGGARAARGTNCARYTNCARGCNTGYNSWTGG	1140
Qy	1069	GCTGACTCTCTGGGGCCCTTCAAGSAGTATATCTCTTTAGTGGAGATGAAAACCGCCCTC	1128
Db	1141	GCNGAYSNYTNCGNCNTTYAARGAYGAYATGYTYNTGTNGARATGAARACNGGNYTN	1200
Qy	1129	AACAACATCAGTCTGTGCTTGGAACCCAGTGGCTGTACACCACCTGCCAGCATGGCC	1188
Db	1201	AAAYAAACNWSNTNTGYGCNTYNGARCCNWSNGSNTGYACNCCNTTNCNWSNTGGCN	1260
Qy	1189	TCCACGAGAGCTGTCTCCCTGGGAGAGGAGTGTCTGCAAGACTTCCGATACACACAGTGT	1248
Db	1261	WSNACNMGNCNGCMGNTYTNNGNGARGARYTNTYTNCARGAYTYTNGNWSNCAYCARGY	1320
Qy	1249	ATGCAGCTGTGGAACAGATGAACAATGGGATCGCTATGGGCTGCCCAATGGAACAAGTAC	1308
Db	1321	ATGCARYTNTGGAAYGAYGAYAAATGGGNWSNYTNTGGCNTGYCCNATGGAYAAARTAY	1380
Qy	1309	ATCCACAGGCGCTGGGTCTAGTATGCTGGCTGGCTGCTACTCTTGGCTGGCGCTTTTC	1368
Db	1381	ATHCAYMGNMNTGGGTNTGNTGTYTNGCNTGYTNTYTNYTNMGNCNGCNGYNTNTTY	1440
Qy	1369	TTCTTCCTCTCTAAAAAGGACCCAGAGAAAGCGGCCCTGGCTCCGCGACGGCTTG	1428
Db	1441	TTTTTYTNTYTNARAARGAYMGNMGNARGCNMGNGENWSNMGACNCGNYTN	1500
Qy	1429	CTCCTCACTCCGCGCAGCGGCTACGAGCGTCTCGTGGGAGCACTGGCGTCCGG	1488
Db	1501	YTYNTNCAYSNCGNAYGGCNGCGNTAYGARMGNYTNGTNGGNCNTYTNCGNWSNCGN	1560
Qy	1489	TTGAGCCAGATGCCACTGCGCGTGGCGGTGGACCTGTGGAGCCGCGCAGCTGAGCGGG	1548
Db	1561	YTNWSNCARATGCCNTMNGNTNGCNGTNGAYTYTNTGWSNMGNGARNTNWSNCGN	1620
Qy	1549	CAGGAGCCCTAGCTGGTTCCACACAGCAGCGCGTATCTGAGGAGGCTGGCGTG	1608
Db	1621	CATGNGCNYTNGTGGTTYCAYCAYCARMGNMGNMGNATHYTNCHARGRGGNGGNTN	1680
Qy	1609	GTAATCTTCTCTTCTCGCCGCGCGGTGGCGAGTGTGAGAGTGGCTGAGCTCCAG	1668
Db	1681	GTNATHYNTNTYWSNCCNCGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCAR	1740
Qy	1669	ACAGTGGAGCCCGGGCCGATGACGCCCTCGCGCTGGCTCAGCTGCGTGTACCCGAT	1728
Db	1741	ACNGTNGARCCNGGNCNCAYGAYGCNTYTNCGNCNTGYTNWSNTGYTNTYTNCCNGAY	1800
Qy	1729	TTCTCTCAAGCGCGGCGAGCCGCGCCTACGTCTGGGGTCTACTTCCAGCGGCTGTGCAAC	1788
Db	1801	TTTTYTNCHARGNMGNCNACNGNMGNTAYGTNGNGTNTAYTYTGYAGGNTYNTNCAY	1860
Qy	1789	CCAGACTCTGTGCCCCCTCCCGTTCGCGCGTCCCGCTCTTCTCCCTGCCCAACGACGTG	1848

Qy 1069 GCTGACTCTCTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAAACCGGCTC 1128
Db 1141 GCNGAYWSNTGNGCNCNTTAAAGYAYATGYTNTGNTGNGARATGAARACNGNGYTN 1200
Qy 1129 AACACACATCAGTCTGCTGCTGGAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1188
Db 1201 AAYAAACNWSNGTNGYGCNTNGARCCNWSNGGTGYACNCNTYTNCCNWSNATGGCN 1260
Qy 1189 TCACGAGAGTGTCTGCTGGGAGAGAGTGTGCTGCAAGACTTCCGATCACACCAAGTGT 1248
Db 1261 WSNACNMGNGCNGCNGMNGTNGGNGARGARYTNTNCARGATYTYMGNWSNCAVCARTGY 1320
Qy 1249 ATGCAGCTGTGGACGATGACACATGCGATGCGTATGSGCCTGCCCATGGAAGTAC 1308
Db 1321 ATGCARVTNTGGAAYGAYAAATGGSNWSNTTNTGGGNTGYCCNATGGAATAY 1380
Qy 1309 ATCCACAGGGCTGGGTCTAGTATGCTGCGCTGCTACTCTTGGCTGGCGCTTTTC 1368
Db 1381 ATHCAYMNGTGGTNTGNTGNTGTYGTYGNTGNTGNTGNTGNTGNTGNTGNTGNTGNT 1440
Qy 1369 TTCTTCTCTCTTAAAGGACCGCAGGAAAGCGGCGCTGCTCCGCAAGCGCTTG 1428
Db 1441 TTYTYYTNTYNTNAARAGAYMGNMNAARCGNCGNMGNSNMGNAACNGCNYTN 1500
Qy 1429 CTCTCCACTCCGCGAGCGGCGCTACGAGGCTGCTGGAGCACTGGGCTCGCG 1488
Db 1501 YTYNTNCAYSNGCNGAYGNGCNGNTAYGARMGNTYNTGNGCNGNTGNGCNGN 1560
Qy 1489 TTGAGCCAGATGCACATGCGCTGCGCTGAGCTGTGGAGCGCGCGAGCTGAGCGG 1548
Db 1561 YTNWSNCRATGCCNTYTMNGTNGCNGTNGAYTYTNGWSNMGNGARYTNWSNCGN 1620
Qy 1549 CACGGAGCCCTAGCTGTGTTCCACACAGCGAGCGCGTATCTTCGAGGAGGTGGCGTG 1608
Db 1621 CAYGNGCNYTNGCTGTTTCAYCAYCARMGNMGNMGNATHYTNCAARGGNGGNTN 1680
Qy 1609 GTATCTCTCTTCTGCGCGCGCGCTGCGGAGTGTGAGAGTGTGCTGAGCTCCAG 1668
Db 1681 GTNATHYNTYNTYWSNCCNGCNGCNGTNGCNCARTGYCARTGGYTNCARYTNCA 1740
Qy 1669 ACAGTGGAGCCGGCGGATGAGCGCTGCGCGCTGCTGAGCTGCGTACCGAT 1728
Db 1741 ACNGTNGARCCNGCNCNCAYGACNYTNGCNGCNGTNGTNGTNGTNGTNGTNGTNG 1800
Qy 1729 TTCTGCAAGCCGGCGGACCGCGCTACGCTGCGGCTCTACTTCAAGCGGCTGCTGCAC 1788
Db 1801 TTYTTCARGNMGNGCNAACNGNMGNTAYGTNGGNTYATYTYGAYGNYTNTNCA 1860
Qy 1789 CAGACTCTGTGCTCCCGTCCGCTGCGGCTGCGCGCTCTTCTCCCTGCGCAGCGAGTG 1848
Db 1861 CNGAYWSNGTNCNWSNCCNTTYMNGTNGCNCNTYTYWSNTYTNCCNWSNCA 1920
Qy 1849 CCGGCTTCTGATGACATGACGAGGAGGCTGTCCACTTTCGCGGGGCGACCCGCGGAC 1908
Db 1921 CNGCNYTYTNGAYGNYTNCARGNGNTGWSNACNWSNCGNNGCNGCNGAY 1980
Qy 1909 CCGGTGGAACAGTGAACCCAGGCGCTGCGCTCCGCTGCGCCTGCAAGCTGTACTTCTAGCTG 1968
Db 1981 MNGTNGARMGNTACNARGCNYTNMGNWSNCGNYTNGAYWSNTGYACNWSNWSN 2040
Qy 1969 GAAGCCCCAGGCTGCTGCGAGGAATGGGACCTGGGACCTGCACTACACTAGAA 2022
Db 2041 GARGCNCNGGNTGYTGARGARTGGGAYTYTNGCNCNTGYACNACNYTNGAR 2094

RESULT 12
AAC85027
ID AAC85027 standard; cDNA; 2255 BP.
XX AC AAC85027;
XX AC
XX AC
DT 08-MAY-2001 (first entry)
XX

DE Human cytokine receptor Zcytor14 encoding cDNA.
XX Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antiinflammatory; gene therapy; vaccine; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
CDS 3..2232
FT FT /*tag= a
FT FT /product= "Zcytor14"
XX
XX WO200104304-A1.
XX 18-JAN-2001.
XX 30-JUN-2000; 2000WO-US018383.
XX 07-JUL-1999; 99US-00348854.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Burkhead SK, Powder SL;
XX WPI; 2001-112618/12.
XX P-PSDB; AAB61880.
XX New polypeptide encoding a human cytokine receptor Zcytor14, for treating
XX inflammation e.g. rheumatoid arthritis.
XX Claim 8; Page 87-91; 112pp; English.
XX The invention provides a new human cytokine receptor designated Zcytor14.
XX Zcytor14 can be expressed by standard recombinant methodology. The
XX encoding nucleic acid is useful for detecting the expression of a
XX Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
XX used to screen biological samples in vitro for the presence of Zcytor14.
XX Proteins, polypeptides and peptides having Zcytor14 activity can be
XX administered to a subject who lacks an adequate amount of this
XX polypeptide, for treating inflammation and conditions such as rheumatoid
XX arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
XX antibodies) can be used to treat a subject who produces an excess of
XX Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
XX the human cytokine receptor Zcytor14
XX
XX Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 U; 0 Other;

Query Match 57.5%; Score 1162.4; DB 4; Length 2255;
Best Local Similarity 75.0%; Pred. No. 2.1e-246;
Matches 1541; Conservative 0; Mismatches 461; Indels 52; Gaps 5;
Qy 1 ATGCGCTGTCTCTGCTTCTGCTGCTTGGCACCTGGGCGGAAACCTGTGCTCTCT 60
Db 154 ATGCGCTGTCTGCTGCTTCTGCTGCTTGGCACCTGGGCGGAAACCTGTGCTCTCT 213
Qy 61 CTGGAGAGACTCATGAGGCTCAGGACACTGACGCTGCTCTCTAGGCTCTCTCTGCCCAC 120
Db 214 CTGGAGAGGCTTGTGGGCTCAGGACGCTACCCACTGCTCTCCGGGCTCTCTCTGCGC 273
Qy 121 CTCTGGATGTGTGAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 274 CTCTGGGACAGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
Qy 181 CTAGTGCCTACCGGCTCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 334 CTGGGCTCTACGACCTTGACAGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 393
Qy 241 GCGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 394 GACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
Qy 301 GAAGTGGAAAGT-----CTGATTTCAGAACTCCAGGAGTCTTAGGAACGCTCT 348

[illegible]

D	b	1531	TGCTACTCTTTGGCGCTGGCGTTTCCGCTCATCTCTCTCAAAAAGATCAACGCGAAA	1590
Q	y	1402	GGGGCCCGTGCTCCGGCAGCGGCTTGCTCTCTCACTCCGCGCAGGAGGGGCTACGAG	1461
D	b	1591	GGGGCGGCAGGGGCGCGGCGCTTGCTCTCTTACTCAGCGGATGACTCGGGTTTCGAG	1650
Q	y	1462	CGTCGTGTGGAGACACTGGCGTCCGCGTTGAGCCAGATGCCACTGCGGTGGCGGTGGAC	1521
D	b	1651	CGCTGTGTGGGCGCCCTGGCGTTCGCGCTGTCAGCTGCGCGTGGCGGTGAGAC	1710
Q	y	1522	CTGTGGAGCGCGCGGAGACTGAGCGCGCAGGAGCCCTAGCTGTTCTCCACACACAGCGA	1581
D	b	1711	CTGTGGAGCGCGTCTGTAATGACTGAGCGCGCAGGGGCGCGGTGTTGTTTTCAGCGCAGCGG	1770
Q	y	1582	CGCCGTATCTGTCAGAGGGGTGGCGTGGTAAATCTCTTCTGTCGCCCGCGCGCGTGGCG	1641
D	b	1771	CGCCAGACCTGACAGAGGGCGGCGTGGTGTCTTGTCTCTCTCCGCGTGGCGTGGCG	1830
Q	y	1642	CAGTGTACAGATGGGTGCA-----GCTCCAGACAGTGGAGCCCGGGCGCGCATGAC	1692
D	b	1831	CTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCGCGCGCGCGCACCGGACGAC	1890
Q	y	1693	GGCTCGCGCGCTGGCTCAGCTGCGTGTCTACCGCGATTTCTGCAGGCGCGCGGACCGGC	1752
D	b	1891	GGCTTCGGGCGCTCGCTCAGCTGGTGTGCTGCCGACTTCTTCAGGGCGCGCGCGCGCGC	1950
Q	y	1753	CGCTACGTGGGGTCTACTTCGACGGGCTGTGCACCCAGACACTCTGTGCGCTCCCGTTTC	1812
D	b	1951	AGCTACGTGGGGCGCTTCGACAGGCTGTCTCACCCGAGCGCGTACCCCGGCGCGCTTTC	2010
Q	y	1813	CGCGTGGCGCGCTCTTCTCCCTGCCCGCAGCAGCTGCCGCGTTTCTGTGATGCACTGCGAG	1872
D	b	2011	CGCACGTGGCGCTCTTACACTGCCCTCCCACTGCCAGACTTCTTGGGGGCGCTTGCAG	2070
Q	y	1873	GGAGGCTGTCTCACTTCCGCGGGGCGACCCGCGGACCGGGTGGAAAGAGTGACCCAGCGG	1932
D	b	2071	CAGCCTCGCGCGCGCGCTTCCGCGCGGCTCCAGAGAGAGCGGAGCGAGTGTCTCCGGGCC	2130
Q	y	1933	CTGGGTCGCCCTCTGGACAGCT-GTACTTCTAGCTGGAGAGCCCGAGGCTGTCTGGAGGA	1991
D	b	2131	CTTCAGCGAGCGCTCTGGATAGCTACTTCCATCCCGCGGAGTCCGCGCGGAGACGCGGG	2190
Q	y	1992	ATGGGACCTGGGAC 2005	
D	b	2191	GTGGGACCGGGGC 2204	
RESULT 13				
AAD47894				
ID	AAD47894 standard; cDNA; 2255 BP.			
XX	AAD47894;			
XX	AC AAD47894;			
DT	12-FEB-2004 (first entry)			
XX	Human cytokine receptor Zcytor14 cDNA.			
DE				
XX				
XX	Cytokine receptor; Zcytor14; chromosome 3p25-3p24; cardiomyopathy;			
KW	xeroderma pigmentosum; Marfan-like connective tissue disorder;			
KW	diabetes mellitus; Panconi anaemia; renal cell carcinoma; gene;			
KW	Marfan syndrome; Von Hippel-Lindau syndrome; blepharophimosis; human; ss.			
XX				
OS	Homo sapiens.			
XX				
Key	Location/Qualifiers			
PH	154..2232			
FT	CDS			
FT	/*tag= a			
FT	/product= "Zcytor14 precursor protein"			
FT	154..213			
FT	/*tag= b			
FT	sig_peptide			
FT	154..213			
FT	mat_peptide			
FT	214..2229			
FT	/*tag= c			
FT	/product= "Mature Zcytor14 protein"			
FT				

Thu Aug 17 14:34:39 2006

Db 1711 CTGTGGAGCCGTCGTGAACAGCGCGCGAGGGCCCGTGGCTTGGTTTCACGGCGACGGG 1770
Qy 1582 CGCCGTATCTCTGACAGAGGGTGGCGTGGTAATCTTCTCTCTCGCCGCGCGCGTGGCG 1641
Db 1771 GCCAGACCTTGCAGAGGGCGGTGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1830
Qy 1642 CAGTCTAGCAGTGTCTGCA-----GCTCCAGACAGTGGAGCCGCGCGCATGAC 1692
Db 1831 CTGTGACGAGTGTCTACAGATGGGGTGTCCGGGGCCCGGGCGCACGGCCCGCACGAC 1890
Qy 1693 GCCCTCGCGCTGCTCAGCTGCTGCTACCCGATTTCTGCAAGCGCGCGCGACCGCG 1752
Db 1891 GCTTTCGGCGCTCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1950
Qy 1753 CGCTAGCTCGGGTCTACTTCAGCGGGTGTGTCACCCAGACTCTGTCCCTCCCGTTC 1812
Db 1951 AGCTAGTGGGGCTGTCTTCAGACGGCTGTCCACCCGGAGCGGTACCCGCCCTTTTC 2010
Qy 1813 CGGCTGCGCGCTCTTCCCTGCCAGCAGCTGCGGGCTTCTCTGATGCACTGCGAG 1872
Db 2011 CGACCGTGGCGCTCTTCACTGCTCCCTCCCACTGCCAGACTTCTTGGGGCCCTGCG 2070
Qy 1873 GGAGGCTGTCTCACTTCCGCGGGCGACCCGCGGAGCGGTGCAAGAGTACCCAGCGG 1932
Db 2071 CAGCTCGCGCCCGCTTCCGGGGCGCTTCCAGAGAGAGCGGAGCAAGTGTCTCCGGGCC 2130
Qy 1933 CTGGGTCCCGCTGACAGCT-GTACTTCTAGCTCGGAAGCCCGAGGCTGTGCGAGGA 1991
Db 2131 CTTTCAGCAGCCCTGGATAGTACTTCTCCATCCCGCGGAGCTCCCGCGCGGGAGCGGG 2190
Qy 1992 ATGGGACTGGGAC 2005
Db 2191 GTGGGACCGGGC 2204
RESULT 14
AF05348
ID AF05348 standard; CDNA; 2255 BP.
XX AC AF05348;
XX DT 23-FEB-2006 (first entry)
XX DE Human IL17A and F receptor zcytor14 cDNA SEQ ID NO 1.
XX KW antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
XX KW antiarthritic; dermatological; antipsoriatic; antibacterial;
XX KW immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
XX KW inflammatory bowel disease; asthma; respiratory disease;
XX KW ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;
XX KW gastrointestinal disease; arthritis; antiarthritic;
XX KW musculoskeletal disease; psoriasis; antipsoriatic;
XX KW dermatological disease; immune disorder; atopic dermatitis;
XX KW dermatological; endotoxemia; inflammation; endotox shock; sepsis;
XX KW antibacterial; immunosuppressive; infection; zcytor14; gene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 154..2232
FT /tag= a
FT /product= "zcytor14x1"
FT FT 214..1509
FT /tag= b
FT /product= "zcytor14x1"
FT /partial
FT /note= "No start or stop codon given"
XX PN WO2005123778-A2.
XX PD 29-DEC-2005.
XX 10-JUN-2005; 2005WO-US020521.
XX , PF

XX PR 10-JUN-2004; 2004US-0578805P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PP Presnell SR, Burrehead SK, Levin SD, Kuestner RE, Gao Z;
XX PI Jaspers SR, Hillsborough J;
XX PS WPI; 2006-067457/07.
XX DR P-PSDB; AEF05349, AEF05350.
XX PT New isolated soluble receptor comprises at least one Zcytor14 subunit,
XX FT useful for treating an inflammatory disease, e.g. asthma, inflammatory
XX FT bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
XX FT psoriasis.
XX PS Example 28; SEQ ID NO 1; 205pp; English.
XX CC The invention describes an isolated soluble receptor comprises at least
XX CC one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
XX CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
XX CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
XX CC ID NO. 24) given in the specification. Also described are: an isolated
XX CC soluble receptor comprising Zcytor14, where Zcytor14 comprises a
XX CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
XX CC the pro-inflammatory activity of either IL-17A comprising fully defined 153
XX CC 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
XX CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
XX CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
XX CC and where the antibody or antibody fragment reduces the pro-inflammatory
XX CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
XX CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
XX CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
XX CC role; and treating a pathological condition in a subject associated with
XX CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
XX CC subunit is useful for treating an inflammatory disease, e.g. asthma;
XX CC chronic inflammatory disease selected from inflammatory bowel disease,
XX CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
XX CC psoriasis; or acute inflammatory disease selected from endotoxemia,
XX CC septicemia, toxic shock syndrome, or infectious disease. This sequence
XX CC represents human IL-17A and IL-17F receptor zcytor14.
XX SQ Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 U; 0 Other;
Query Match 57.5%; Score 1162.4; DB 15; Length 2255;
Best Local Similarity 75.0%; Pred. No. 2.1e-246;
Matches 1541; Conservative 0; Mismatches 461; Indels 52; Gaps 5;
Qy 1 ATGCCCTGTCTCTGTTCTCTGCTGCTTGGCAGCTGGGCGCGAAACCTGTGCTCTCTCT 60
Db 154 ATGCCCTGTCTCTGTTCTCTGCTGCTTGGCAGCTGGGCGCGAAACCTGTGCTCTCTCT 213
Qy 61 CTGGAGAGCTGATGGAGCTCAGGACATGACGCTGCTCTAGGCTCTCTCTCTCTCTCTCT 120
Db 214 CTGGAGAGCTTGTGGGGCTCAGGACGCTACCCAGCTGCTCTCCGGGCTCTCTCTCTCT 273
Qy 121 CTCTGGAGTGTGACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 274 CTCTGGGACAGTGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
Qy 181 CTAGTGTCTACCCGCTCTGACAGCGGAGCTGGTGTCTCAGGTGCTCAAGAGACAGATTGC 240
Db 334 CTGGCGCTACGACCTGACAGAGCTGGTGTCTCAGGTGCTCAAGAGAGAGCCGACTGT 393
Qy 241 GCCCTCCGTCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 394 GACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
Qy 301 GAAGCTGGAAGT-----CTGATTTCAGAACTCCAGAGTCTAGAGACGCTCT 348
Db 454 GATGAGGAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCCTAGGAAATGCTCT 513
Qy 349 CTCAGGCGCCAGGTGGTGTCTCTCTCCAGGCTACCCCATCGCCGCTGTGCTGCTGCTG 408

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2006, 21:03:24 ; Search time 9736 Seconds
(without alignments)
11613.485 Million cell updates/sec

Title: US-10-719-202-1_COPY_197_2218
Perfect score: 2022
Sequence: 1 atgctgtgtctgtgtcttct.....gacctgtcactacactagaa 2022

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_estc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1561.6	77.2	1762	6 AK075634	AK075634 Mus muscu
2	813.8	40.2	1039	1 AV010326	AV010326 AV010326
3	754.2	37.3	850	3 BQ949741	BQ949741 AGENCOURT
4	681.8	33.7	697	2 B1332055	B1332055 AGENCOURT
5	668.2	33.0	900	10 DV727885	DV727885 RVL20458
6	643.2	31.8	775	1 AI007139	AI007139 ua81f02.r
7	628.4	31.1	784	2 BG968034	BG968034 602832412
8	620.4	30.7	973	6 AK040950	AK040950 Mus muscu
9	620.4	30.7	3710	6 AK033890	AK033890 Mus muscu
10	612.4	30.3	722	7 BF237179	BF237179 602028133
11	593.8	29.4	597	3 BQ829429	BQ829429 LL6in2310
12	591.2	29.2	643	7 BG625706	BG625706 BG625706
13	573.4	28.4	620	7 BG637050	BG637050 BG637050
14	569.4	28.2	739	5 CK474183	CK474183 AGENCOURT
15	564.4	27.9	847	9 CX756755	CX756755 AGENCOURT
16	562	27.8	562	7 BE290565	BE290565 601089427
17	555.8	27.5	1006	7 BG609618	BG609618 BG609618
18	554	27.4	635	7 BF160122	BF160122 601767822
19	553.4	27.4	594	3 BM729443	BM729443 ih81a09.x

20	553.4	27.4	839	2	BI251117	BI251117 602994315
21	546.2	27.0	679	3	BQ192107	BQ192107 UI-R-DRI-
22	542.4	26.8	628	3	BP769075	BP769075 BP769075
23	507.8	25.1	1040	3	BQ951730	BQ951730 AGENCOURT
24	503.8	24.9	628	3	BQ210030	BQ210030 UI-R-EP0-
25	501.2	24.8	884	5	CK770217	CK770217 958358 MA
26	499	24.7	619	2	BI282622	BI282622 UI-R-CW08
27	499	24.7	830	9	CX867569	CX867569 HESCA 22
28	498.8	24.7	1060	3	BUS23068	BUS23068 AGENCOURT
29	479.8	23.7	653	7	BF161982	BF161982 601767930
30	477	23.6	609	11	AZ995676	AZ995676 2M0281A07
31	477	23.6	1024	3	BQ953658	BQ953658 AGENCOURT
32	476.2	23.6	982	3	BM608181	BM608181 AGENCOURT
33	475.2	23.5	831	5	CK772940	CK772940 961525 MA
34	472.6	23.4	515	5	CJ237410	CJ237410 CJ237410
35	471.6	23.3	499	5	CJ194228	CJ194228 CJ194228
36	464.6	23.0	829	2	BI689749	BI689749 603316255
37	454.4	22.5	787	2	BG917539	BG917539 602817086
38	448.4	22.2	1118	10	WI3694	WI3694 ma94902.r1
39	445.6	22.0	702	2	BM009552	BM009552 603630118
40	444.4	22.0	757	9	CX867488	CX867488 HESCA 22
41	444.2	22.0	771	5	CK774755	CK774755 963540 MA
42	442.6	21.9	932	3	BQ962425	BQ962425 AGENCOURT
43	438.4	21.7	526	2	BI413402	BI413402 602986759
44	436.8	21.6	1086	3	BM920537	BM920537 AGENCOURT
45	436.4	21.6	459	4	BY598683	BY598683 BY598683

ALIGNMENTS

RESULT 1	AK075634	1762 bp	linear	HTC 02-SEP-2005
LOCUS	AK075634	Mus musculus 18-day embryo whole body cDNA, RIKEN full-length		
DEFINITION	AK075634	enriched library, clone:110025H02 product:hypothetical protein, full insert sequence.		
ACCESSION	AK075634			
VERSION	AK075634.1	GI:26344438		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1	Carninci, P. and Hayashizaki, Y.		
AUTHORS		High-efficiency full-length cDNA cloning		
TITLE		Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL		10349636		
PUBMED				
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS		Normalization and subtraction of cap-trapper-selected cDNAs to		
TITLE		prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED		11042159		
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kawai, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
AUTHORS		RIKEN integrated sequence analysis (RISA) system--384-format		
TITLE		sequencing pipeline with 384 multicapillary sequencer		
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED		11076861		
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
AUTHORS		Functional annotation of a full-length mouse cDNA collection		
TITLE				

JOURNAL REFERENCE AUTHORS	Nature 409, 685-690 (2001)	Best Local Similarity 95.5%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 5; Indels 73; Gaps 2;
TITLE	The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL REFERENCE AUTHORS	Nature 420, 563-573 (2002)	
TITLE	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome	
JOURNAL REFERENCE AUTHORS	Science 309, 1564-1566 (2005)	
TITLE	The PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). The Transcriptional Landscape of the Mammalian Genome	
JOURNAL REFERENCE AUTHORS	Science 309, 1559-1563 (2005) (bases 1 to 1762)	
TITLE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission	
TITLE JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. 1762 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:1110025H02" /db_xref="taxon:10090" /clone="1110025H02" /tissue type="whole body" /clone lib="RIKEN full-length enriched mouse cDNA library" /dev stage="18-day embryo" 817..1743 /note="unnamed protein product; hypothetical protein (evidence: decoder) putative" /codon_start=1 /protein_id="BAC35870.1" /db_xref="GI:26344439" /translation="MLLYEMKTLNNTSVCALEPSGCTPLPMSASTRAARLGEELLQD FRSHQCMQNDNNGSLWACENDKIHRRWVWLVWLACILLAAALFFPLLKQPRKA ARGSTALLSHDAGYERLVGALASQMPKLVAVDLMSRELSSAHGALWPHHQ RRRILOEGVWLLFSPAACQQLQVTEPGPHDAAWLSCLVPDFQGRATG RVGVYFDGLHPDVPSPFRVAPLPSLPQLPDLALQGCSTSGRPAEDRVERVT QALRSALDSCTSSSEAPGCCBWDLPCTTLE"	
FEATURES source		
CDS		
ORIGIN		
Query Match	77.2%; Score 1561.6; DB 6; Length 1762;	

Db 1026 CATCCACAGGCGCTGGTCTTAGTATAGTGGCTGCGCTACTCTTGGCTGGCGGCTTTT 1085

Qy 1368 CTTCTTCTCTCTTCTTAAAGAGGACCGCAGGAAAGCGGCGCGTGGCTCCGCGACGCGCTT 1427

Db 1086 CTTCTTCTCTCTCTTCTTAAAGAGGACCGCAGGAAAGCGGCGCGTGGCTCCGCGACGCGCTT 1145

Qy 1428 GCTCTCTCACTCCGCGGAGCGGCTTACGAGGCTCTGGTGGAGCACTGGCTCCGC 1487

Db 1146 GCTCTCTCACTCCGCGGAGCGGCTTACGAGGCTCTGGTGGAGCACTGGCTCCGC 1205

Qy 1488 GTTAGGACAGATGCCACTGCGCTGGCGGCTGACCTGTGGAGCGCGCGGAGCTGAGCGC 1547

Db 1206 GTTAGGACAGATGCCACTGCGCTGGCGGCTGACCTGTGGAGCGCGCGGAGCTGAGCGC 1265

Qy 1548 GCACGAGCCCTAGCTGTGTTCCACACAGCAGCGCGGTATCTTGCAGGAGGGTGGCGT 1607

Db 1266 GCACGAGCCCTAGCTGTGTTCCACACAGCAGCGCGGTATCTTGCAGGAGGGTGGCGT 1325

Qy 1608 GGTATATCTTCTTCTTCTGCGCGCGGCGGCTGAGCTGTGAGCTGTGCTGAGCTTCA 1667

Db 1326 GGTATATCTTCTTCTTCTGCGCGCGGCGGCTGAGCTGTGAGCTGTGCTGAGCTTCA 1385

Qy 1668 GACAGTGGAGCCCGCGCGCATGAGCGCTGCGCGCGGCTGAGCTGTGCTGAGCTTCA 1727

Db 1386 GACAGTGGAGCCCGCGCGCATGAGCGCTGCGCGCGGCTGAGCTGTGCTGAGCTTCA 1445

Qy 1728 TTTCTTGCAGGCGCGGCGGACCGCGCTAGCTGCGGCGTCTACTTTCGAGCGGCTGCTGCA 1787

Db 1446 TTTCTTGCAGGCGCGGCGGACCGCGCTAGCTGCGGCGTCTACTTTCGAGCGGCTGCTGCA 1505

Qy 1788 CCAGACTGTGCGCTTCCCGTTCGCGGCTGCGCGGCTTCTTCTTCCGCGGCTGCGAGCT 1847

Db 1506 CCAGACTGTGCGCTTCCCGTTCGCGGCTGCGCGGCTTCTTCTTCCGCGGCTGCGAGCT 1565

Qy 1848 GCGGCTTCTTCTGATGCACTGACGAGGAGTGTCTTCTTCCGCGGCGGCGGCGGCA 1907

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Qy 1968 GGAAGCCCGAGCTGCTGCGAGGAATGGAGCTGGGACCTTGGCACTACTAGAA 2022

Db 1686 GGAAGCCCGAGCTGCTGCGAGGAATGGAGCTGGGACCTTGGCACTACTAGAA 1740

RESULT 2

AV010326

LOCUS AV010326 Mus musculus 1039 bp mRNA linear EST 23-OCT-2001

DEFINITION clone 1110025H02, mRNA sequence.

ACCESSION AV010326

VERSION AV010326.2 GI:16356130

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT On May 11, 1999 this sequence version replaced gi:4787313. Contact: Chie Owa Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@tc.riken.go.jp

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

FEATURES

Location/Qualifiers

1..1039
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1110025H02"
/sex="mixed"
/dev_stage="18-day embryo"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"

ORIGIN

Query Match 40.2%; Score 813.8; DB 1; Length 1039;
Best Local Similarity 96.9%; Pred. No. 2.9e-186;
Matches 883; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

Qy 1113 GATCAAAACCGGCTCAACACACATCAGTCTGTGCGCTTGGAAACCCAGTGGCTGTACACC 1172

Db 112 GAATGAACACCGGCTCAACACACATCAGTCTCTGC--TTGGAACACCGTGTGTACACA 169

Qy 1173 ACTGCCAGCATGCGCTCC--ACGAGAGTGTCTCGCTGGGAGAGAGTGTGTGCAAGACT 1231

Db 170 CTTGCCGAGCATGCGCTCCAAACGAGAGTGTCTCGCTGGAGAGAGTGTGTGCAAGACT 229

Qy 1232 TCCGATCACACACAGTGTATGAGCTGTGGACGATGACACATGCGTATGCGTATGGGCT 1291

Db 230 CCGGATCACACACAGTGTATGAGCTGTGGACGATGACACAT--GGATCGCTAT--GGCT 287

Qy 1292 GCCCATGGACAAGTATACATCACAGGCGCTGGGCTCTAGTATGCTGGCTTCTCTACTCT 1351

Db 288 GCCCATGGACAAGTATACATCACAGGCGCTGGGCTCTAGTATGCTGGCTTCTCTACTCT 347

Qy 1352 TGGCTGGGCGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1411

Db 348 TGGCTGGGCGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 407

Qy 1412 GCTCCCGACGCGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1471

Db 408 GCTCCCGACGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 467

[illegible]

prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES	Location/Qualifiers	1..973	misc_feature	1..973	Query Match	Best Local Similarity	Matches	Conservative	Score	DB 6;	Length	973;	Indels	0;	Gaps	0;
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ORIGIN																
QY	1401	AGCGGCGCGTGGCTCCCGCACGCGCTTGTCTCCCTCCACTCCGCGGAGCGGGCTAGCA	611													
Db	670	AGCGGCGCGTGGCTCCCGCACGCGCTTGTCTCCCTCCACTCCGCGGAGCGGGCTAGCA	611													
QY	1461	GGCTCTGGTGGAGCACTGGCGTCCGCTGTAGCCAGATGCCACTGCGCGTGGCGGTGGA	1520													
Db	610	GGCTCTGGTGGAGCACTGGCGTCCGCTGTAGCCAGATGCCACTGCGCGTGGCGGTGGA	551													
QY	1521	CTGTGCGAGCGCGCGAGCTGAGCGCGCACGAGCGCTTAGCCTGGTTCACACACGCG	1580													
Db	550	CTGTGCGAGCGCGCGAGCTGAGCGCGCACGAGCGCTTAGCCTGGTTCACACACGCG	491													
QY	1581	ACGCGGTATCTCGAGAGGGTGGCTGGTGTATCTCTCTCTCGCCCGCGCGCGCTGCG	1640													
Db	490	ACGCGGTATCTCGAGAGGGTGGCTGGTGTATCTCTCTCTCTCGCCCGCGCGCGCTGCG	431													
QY	1641	GCAGTGTACAGTGGCTGCAGCTCCAGACAGTGGAGCGCGCGCGCGCATGACGCTCGC	1700													
Db	430	GCAGTGTACAGTGGCTGCAGCTCCAGACAGTGGAGCGCGCGCGCGCATGACGCTCGC	371													
QY	1701	CGCTGTGCTCAGTGGCTGTCTACCCGATTTCTGCAAGCGCGCGCGCGCTACGCT	1760													
Db	370	CGCTGTGCTCAGTGGCTGTCTACCCGATTTCTGCAAGCGCGCGCGCGCTACGCT	311													
QY	1761	CGGGTCTACTTCCGACGGGCTGTGTCACCCAGACTCTGTGCTTCCCGTTCGCGCTCGC	1820													
Db	310	CGGGTCTACTTCCGACGGGCTGTGTCACCCAGACTCTGTGCTTCCCGTTCGCGCTCGC	251													
QY	1821	CCCGCTCTTCTCCCTCCGACGAGTGGCGGCTTCTCGATGCTACTGACGAGGAGCTG	1880													
Db	250	CCCGCTCTTCTCCCTCCGACGAGTGGCGGCTTCTCGATGCTACTGACGAGGAGCTG	191													
QY	1881	CTTCACATTTCCGCGGGGACCCCGGACCCGGGTGGAGAGTACCCAGGCGCTCGGTC	1940													
Db	190	CTTCACATTTCCGCGGGGACCCCGGACCCGGGTGGAGAGTACCCAGGCGCTCGGTC	131													
QY	1941	CGCCCTGGACAGCTGTACTTTCTAGCTCGGAGACCCCGAGCTGCTCGAGGAATGGACCT	2000													
Db	130	CGCCCTGGACAGCTGTACTTTCTAGCTCGGAGACCCCGAGCTGCTCGAGGAATGGACCT	71													
QY	2001	GGGACCTCGACTACACTAGAA	2022													
Db	70	GGGACCTCGACTACACTAGAA	49													
RESULT 9																
AK033890/c																
LOCUS																

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
Antisense transcription in the Mammalian Transcriptome
Science 309, 1564-1566 (2005)

7 The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)

8 (bases 1 to 973)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

COMMENT

DEFINITION	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330110N14 product:unclassified, full insert sequence.
ACCESSION	AK033890
VERSION	AK033890.1 GI:26083639
KEYWORDS	HTC; CAP trapper;
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sasaki, N., Carninci, P., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBMED	
REFERENCE	5
AUTHORS	The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBMED	
REFERENCE	6
AUTHORS	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE	Antisense Transcription in the Mammalian Transcriptome
JOURNAL	Science 309, 1564-1566 (2005)
PUBMED	
REFERENCE	7
AUTHORS	The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE	The Transcriptional Landscape of the Mammalian Genome
JOURNAL	Science 309, 1559-1563 (2005)
PUBMED	
REFERENCE	8 (bases 1 to 3710)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takanashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

COMMENT

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, Tel.81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES

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REFERENCE			
AUTHORS	Hackney,J.A., Charbord,P., Brunk,B.P., Stoeckert,C.J., Lemischka,I.R. and Moore,K.A.		
TITLE	A molecular profile of a hematopoietic stem cell niche		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066		(2002)
PUBMED	12226475		
COMMENT	Contact: Moore, Kateri A. Department of Molecular Biology Princeton University 217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA Tel: 609 258 0605 Fax: 609 258 2759 Email: kmoore@molbio.princeton.edu These ESTs are derived from a subtracted cDNA library enriched for gene products expressed by a hematopoietic stem cell-supporting stromal cell line, AFT024. Seq primer: M13Reverse or T7. Location/Qualifiers 1. 597 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /tissue_type="Fetal Liver" /cell_type="Stromal cell" /cell_line="AFT024" /dev_stage="Embryonic day 14-14.5" /lab_host="DH10B" /clone_lib="AFT024-subtracted library" /note="Organ: Fetal Liver; Vector: Sport 1; Site 1: Sal 1; Site 2: Not 1; Two directionally cloned cDNA libraries were made from a hematopoietic stem cell-supporting stromal cell line (AFT024) and from a non-supporting stromal cell line (2018). Subtractive hybridization was performed by hybridization of the target. AFT024, single		
FEATURES			
source			

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AUTHORS			
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COMMENT			
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Fax: 81-45-503-9216
Email: genome-rc@gs.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

ACCESSION	DB	SEQUENCE
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National Institutes of Health, Mammalian Gene Collection (MGC)	QY	361 GTGGTGCTCTCTCTCCAGGCCCTACCCCATCGCCCGCTGTGCCCTGTCTGGAGGTCCAGGTG 420
Unpublished (1999)		
Contact: Daniela S. Gerhard, Ph.D.	Db	534 GTGGTGCTCTCTCTCCAGGCCCTACCCCATCGCCCGCTGTGCCCTGTCTGGAGGTCCAGGTG 593
Office of Cancer Genomics		
National Cancer Institute / NIH	QY	421 CCGCTGACCTCGTGCAGCCTCGTCAGTCCGTTGGGTCTCTGGGTATTTGACTGTTTCGAG 480
Bldg. 31 Rm10A07 Bethesda, MD 20892		
Email: cga@nci.nih.gov	Db	594 CCGCTGACCTCGTGCAGCCTCGTCAGTCCGTTGGGTCTCTGGGTATTTGACTGTTTCGAG 653
Tissue Procurement: Meri Firpo		
cDNA Library Preparation: Express Genomics	QY	481 GCTAGTCTTTGGGGGCTGAGGTACAGATCTGGTCTTACACGAAAGCCCGAGGTACACGAAAGAG 540
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
DNA sequencing by: Agencourt Bioscience Corporation	Db	654 GCTAGTCTTTGGGGGCTGAGGTACAGATCTGGTCTTACACGAAAGCCCGAGGTACACGAAAGAG 713
Clone distribution: MGC clone distribution information can be		
found through the I.M.A.G.E. Consortium/LLNL at:	QY	541 CTCAACTCTACACAGCAGCTGCCTGA 566
http://image.llnl.gov		
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GenCore version 5.1.9
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Scoring table: IDENTITY NUC

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	62	3.1	12438	3	US-09-949-016-16581
6	62	3.1	16321	3	US-09-949-016-12490
7	54	2.7	7950	4	US-09-902-540-934
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C 38	48.4	2.4	10596	2	US-07-884-811-15	Sequence 15, Appli
C 39	48.4	2.4	10596	2	US-07-885-971-15	Sequence 15, Appli
C 40	48.4	2.4	10596	2	US-08-087-783A-15	Sequence 15, Appli
C 41	48.4	2.4	10596	2	US-08-194-088B-15	Sequence 15, Appli
C 42	48.4	2.4	10596	2	US-08-194-087-15	Sequence 15, Appli
C 43	48.4	2.4	10596	7	PCT-US93-04648-15	Sequence 15, Appli
C 44	48.4	2.4	16080	3	US-09-724-566A-48	Sequence 48, Appli
C 45	48.4	2.4	16080	3	US-09-471-669A-48	Sequence 48, Appli

ALIGNMENTS

RESULT 1

US-09-747-259-13

- Sequence 13, Application US/09747259
- Patent No. 6569645
- GENERAL INFORMATION:
- APPLICANT: Genentech, Inc.
- APPLICANT: Chen, Jian
- APPLICANT: Filvaroff, Ellen
- APPLICANT: Fong, Sherman
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul
- APPLICANT: Grimaldi, Christopher
- APPLICANT: Gurney, Austin
- APPLICANT: Li, Hanzhong
- APPLICANT: Hillan, Kenneth
- APPLICANT: Tumas, Daniel
- APPLICANT: VanLookeren, Menno
- APPLICANT: Vandlen, Richard
- APPLICANT: Watanabe, Colin
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William
- APPLICANT: Yansura, Daniel
- TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
- FILE REFERENCE: P1381R1C1P1 (US)
- CURRENT APPLICATION NUMBER: US/09/747,259
- CURRENT FILING DATE: 2000-12-20
- PRIOR APPLICATION NUMBER: US 09/311,832
- PRIOR FILING DATE: 1999-05-14
- PRIOR APPLICATION NUMBER: US 60/172,096
- PRIOR FILING DATE: 1999-12-23
- PRIOR APPLICATION NUMBER: PCT/US99/31274
- PRIOR FILING DATE: 1999-12-30
- PRIOR APPLICATION NUMBER: US 60/175,481
- PRIOR FILING DATE: 2000-01-11
- PRIOR APPLICATION NUMBER: PCT/US00/04341
- PRIOR FILING DATE: 2000-02-18
- PRIOR APPLICATION NUMBER: PCT/US00/05841
- PRIOR FILING DATE: 2000-03-02
- PRIOR APPLICATION NUMBER: US 60/191,007
- PRIOR FILING DATE: 2000-03-21
- PRIOR APPLICATION NUMBER: PCT/US00/07532
- PRIOR FILING DATE: 2000-03-21
- PRIOR APPLICATION NUMBER: PCT/US00/15264
- PRIOR FILING DATE: 2000-06-02
- PRIOR APPLICATION NUMBER: US 60/213,087
- PRIOR FILING DATE: 2000-06-22

Qy 1774 GACGGGCTGTCACACAGACTCTGTGCTCCCTCCCGTTCCGCGTTCGCGCCGCTCTTCTCC 1833
 Db 2090 GACAGGCTGCTCCACCGGACCGGTATCCCGCCCTTTTCCGACCGTCCCGTCTTCCACA 2149
 Qy 1834 CTGCGCCAGGAGCTGCGGCTTTCTGATGCACTGACGAGGAGGCTGCTCCACTTCCGG 1893
 Db 2150 CTGCGCTCCCAACTGCGAGACTTCTTGGGGGCTTCCGAGAGGCTTCCGAGAGGCTTCC 2209
 Qy 1894 GGGCGACCGCGGACCGGCTGGAACGAGTGAACCCAGGCGCTGCGGTCGCGCCCTGGAAGC 1953
 Db 2210 GGGCGGCTCCAGAGAGCGGAGCAAGTGTCCCGGGCTTCCAGCCAGCCCTGGATAGC 2269
 Qy 1954 T-GTACTTCTAGCTCGGAAGCCCGAGGCTGCTGCGAGGAATGGAGCTTGGAGC 2005
 Db 2270 TACTTCCATCCCGCGGAGCTCCCGCGCGGAGCGCGGGTGGAGCCAGGGGC 2322

RESULT 2
 US-10-104-047-1326
 ; Sequence 1326, Application US/10104047
 ; Patent No. 6943241
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. 6943241el full length cDNA
 ; FILE REFERENCE: HI-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1326
 ; LENGTH: 2622
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-104-047-1326

Query Match 48.7%; Score 985; DB 3; Length 2622;
 Best Local Similarity 70.7%; Pred. No. 3,46-233;
 Matches 1463; Conservative 0; Mismatches 470; Indels 136; Gaps 6;

Qy 70 CTGATGAGGCTCAGGACACTGCAAGCTGCTCTAGGCTCTCTGAGGCTCTCTGCGACCTCTGGAT 129
 Db 502 CTGGAGGGTCTGGGAATACGGAGCCCGAGAAAGGGCTCTCTGCGGCTCTGGGAC 561
 Qy 130 GGTGACGTGCTCTGCTGCTGGAAGCTCCAGTCTGCGCCAGGCTCTGCTAGTGCCT 189
 Db 562 AGTGACATCTCTGCTGCTGCGGACATCTGCTCTGCTGCGGCTCTGCTGCGGCT 621
 Qy 190 ACCGCTGCGAGCGGAGCTGCTGCTGAGGTGTCCAGAGAGACAGATTGCGGCTCCGT 249
 Db 622 ACGACCTGCGAGAGAGCTGCTGCTGAGTGTCCAGAGAGAGACCGACTGTGACCTCTGT 681
 Qy 250 GTGCGTGTGTGTCCTCTGCGGCTGAGTGGGCACTGGGAGAGCTTGAAGAGCTGGA 309
 Db 682 CTGCGTGTGTGTCCTCTGCGGCTGAGTGGGCACTGGGAGAGCTTGAAGATGAGAA 741
 Qy 310 AGT-----CTGATTCAAGACTCCAGAGTCTAGGAGCGCTCTCTCCAGGCC 357
 Db 742 AGTTTGGAGAGAGCTGACTTGGGGTGGAGAGCTAGGAATGCTCTCTCCAGGCC 801
 Qy 358 CAGTGTGTGCTCTCTTCCAGGCTTACCCATCGCGCTGTGCTGCTGCTGAGGCTCCAG 417
 Db 802 CAGTGTGTCTCTCTTCCAGGCTTACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
 Qy 418 GTGCGGCTGACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
 Db 862 GTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
 Qy 478 GAGGCTAGTCTTGGGCTGAGGTACAGATCTGCTTACAGAGAGCCAGGTACAGAA 537
 Db 922 GAGGCTGCTGAGGAGTGAAGTACGAATCTGCTTATCTGCTTATCTAGCCCGGAGTACGAGAG 981

Qy 538 GAGCTCAACCTTCACACAGCAGCTGCT----- 564
 Db 982 GAACTCAACACACACAGCAGCTGCTGCTGAGGGGCTCGAAGTCTGGAACAGCATC 1041
 Qy 565 -----GATGGTGACAAATGCTCTCTG 585
 Db 1042 CGAGCTGTGGGCCCTGCTGCTGCTCAACGTGTACAGAGATGTTGACAACTGATCTG 1101
 Qy 586 ACACTGATGTCTCTGAGGAGCAGGACTTTAGCTTTCTTACTGTACCTGCTGCTGCTGCTG 645
 Db 1102 GTTCTGAATGTCTCTGAGGAGCAGCACTTCCGCTCTCTCTGTACTGGAATCAGGCTCAG 1161
 Qy 646 GATGCTCTCAAACTCTGTGTGTTGTTCAAAAACCTGACTGGAACCTGATCTTAAAC 705
 Db 1162 GGGCCCCCAAAACCCCGGTGGCAAAAACCTGACTGGAACCCGAGATCATTTACCTTGAAC 1221
 Qy 706 CACACAGACTGCTTCCCTGCTCTGCAATTCAGGTGTGTGCTAGAGCCAGACTCTGAG 765
 Db 1222 CACACAGACTGCTTCCCTGCTCTGTAATTCAGGTGTGCTGCTGGAACCTGACTCCGTT 1281
 Qy 766 AGGTCGAATTTCTGCCCCCTTCCGCGAAGATCCCGGTGCAACAGGAACTCTGCGCACATA 825
 Db 1282 AGGACGAACATCTGCCCCCTTCCAGGAGGAGACCCCGCGCAACACAGAACTCTGCGAAGCC 1341
 Qy 826 GCAGGCTCGGCTACTGCTCCAGGGGTATGGCAGCTAGATGCGCTTGTCTGCTGCTG 885
 Db 1342 GCGCGACTGCACTGCTGACCTTGCAGAGCTGGCTGCTGGAACCGCTGCTGCTGCTGCTG 1401
 Qy 886 GGCAGGTAACTGCTGCTGGCAGGCAACAGACCAGAGTCCCTGCGCAGCACTTGTGCA 945
 Db 1402 GCAGAGCGGCACTGCTGCTGGCGGCTCCGGGTGGGAGACCCCTGCGAGCACTTGTGCTCA 1461
 Qy 946 CCACTGCCCGAGAAACCGCACTGTGAATGAGCCACAAAGATTTCCAGTTGTGGCGAGCC 1005
 Db 1462 CCGCTTCTGCGAGAAATGTCACTGTGGACAGGTTCTCGAGTTCCTTCTGTAAGGC 1521
 Qy 1006 CACCCCAACCTCTGTGTCAGGTGAGCACTGGGAGAAAGTTGAGCTGCAAGGCTGCTG 1065
 Db 1522 CACCTTAACTCTGTGTTCAAGTGAACAGCTGCGAGAGCTGCTGCGAGGAGTCTG 1581
 Qy 1066 TGGGCTGACTCTTGGGGGCTTCAAGGATGATGCTGTAGTGAGATGAAACCGCC 1125
 Db 1582 TGGGCTGACTCTTGGGGGCTTCTCAAGAGAGATGTGCTACTTGTGGAGACAACGAGGCC 1641
 Qy 1126 CTCAACAAACATCACTGCTGCTTGGAAACCCAGTGGCTGTACACACACTGCCAGCATG 1185
 Db 1642 CAGGACAAAGATCCCTCTGCTTGGAAACCCAGTGGCTGTACTTCACTACCCAGCAA 1701
 Qy 1186 GCTTCCACAGAGCTGCTGCTGCGCTGGGAGAGGAGTTGCTGCAAGACTTCCGATCACAC 1245
 Db 1702 GCTTCCACAGAGGAGCTGCTGCTTGGAGAGTACTTACTACAAGACCTGCACTCAGGCC 1761
 Qy 1246 TGTATGACGTGTGGAAACGATGACATGGGATCGCTATGGGCTGCGCCCTGAGCAAG 1305
 Db 1762 TGTCTGACGTATGGGAGCATG---ACTTGGGAGGCTATGCGCTGCTGCTGCTGCTGCT 1818
 Qy 1306 TACATCCACAGGCGCTGCGCTCTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1365
 Db 1819 TACATCCACAGGCTGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1878
 Qy 1366 TTCTTCTTCTCTTCAAAAAGGACCGAGGAA----- 1401
 Db 1879 TCCCTCATCTCTCTCTCAAAAAGGATCACGGAAGAGGTGGCTGAGGCTCTTGAACAG 1938
 Qy 1402 -----CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
 Db 1939 GAGTCCGCTGCGGGGCGGCGCGCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998
 Qy 1447 GAGGCGGCTTACGAGGCTCTGCTGCGGAGCACTGCGCTGCGCTGCGCTGCGCTGCGCTGCT 1506
 Db 1999 GACTCGGCTTTCAGAGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2058

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1507 GCGTGGCCGTGGACCTGTGTGAGCCGCGGAGCTGAGCGCGACGAGCCCTAGCTGG 1566
 2059 GCGTGGCCGTGGACCTGTGTGAGCCGCGTGTAACTGAGCGCGCAGGGCCGTGGCTGG 2118
 1567 TTCCACACACGAGCGAGCGGTATCTCTGAGGAGGCTGGTGTAACTCTCTCTCTCTG 1626
 2119 TTTACGGCGAGCGGCGCAGACCTTGACGAGGCGGCGTGTGTCTTGTCTCTCTCT 2178
 1627 CCCGCGCGGTGGCGACGTGTACAGTGGCTGCA-----GCTCCAGACAGTGGAG 1677
 2179 CCCGCTGGGTGGCGCTGTGACGAGTGGCTACAGGATGGGGTGTCCGGCCCGGGCG 2238
 1678 CCCGGGCGCATGACGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737
 2239 CACGGCCCGCAGACGCTTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2298
 1738 GCGCGGCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1797
 2299 GCGCGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2358
 1798 GTGCCCTCCCGCTTCCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1857
 2359 GTACCGCGCTTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2418
 1858 CTGGATGCTACTGACGAGGAGCTGCTTCCACTTCCGCGGCGGCGACCGCGCGACCGGGTGAA 1917
 2419 CTGGGGCGCTGACGAGCGCTGCTGCGCGCGCGCTTCCGCGCGCTCCAGAGAGAGCGGAG 2478
 1918 CGAGTACCGAGCGCTGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1976
 2479 CAAGTGTCCCGCGCGCTTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2538
 1977 AGCTGTGCTGAGGAGTGGGACCTGGAC 2005
 2539 GCGCGGCGACCGGGTGGGACCGAGGGC 2567

RESULT 3

US-09-949-016-4839
 ; Sequence 4839, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4839
 ; LENGTH: 4076
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-4839

Query Match 3.1%; Score 62; DB 3; Length 4076;
 Best Local Similarity 47.2%; Pred. No. 2.9e-05;
 Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;
 1463 GTCTGTGGGAGCACTGGCGTGTGAGCCAGATGCCACTGGCGGTGGCGCTGGGAC 1522
 1443 GCGTGGAGTGGCCACCGGGCGCTTGGAGGCGCTGGAGGCTTCTTGGAGGTCTGGCAC 1502
 1523 TGTGGAGCGCGCGAGCTGAGCGCGCAGCGAGCCTAGCTGCTTCCACACAGCGAC 1582
 1503 TGCAGGGCAACCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562

1583 GCGGTATCTGACGAGGGTGGTAACTCTTCTGCGCCGCGCGCTGGCGC 1642
 1563 GCGTCAATCTTGGCCGAGAACCGCCTGAGCCACTTCCCGCTGGACACAGGCTGTGTAC 1622
 1643 AGTGTGACGAGTGGCTGACGCTCCAGACAGTGGAGCCCGGGCGCATGACGCCCTGGCG 1702
 1623 TGAGGTGTGGACCTGCGAACAACAGCTTCAGCTCTCTGCGAGGAGTGCATGGGTG 1682
 1703 CTTGGCTCAGCTGCTGCTACCGGATTTCTTGCAGAGCGCGCGCTACGCTG 1762
 1683 GCGTGGAGACCAAGCCTCCGCGCTTACTCTGAGGGGAATCCACTCAGCTGCTGGGCA 1742
 1763 GGTGTACTTCCAGCGGCTGCTGACCCAGACTCTGTGCTTCCCGGTTCGCGTGGCC 1822
 1743 ATGGCTGGCTGGCAGCCAGCTGACAGGCGCTGTGGACGTGGACGCGCACCCAGGACC 1802
 1823 CGCTCTTCTCTCCGCGCGCTGCGAGCTGCGCGCTTCTG 1860
 1803 TGAATCGCGCTTCACTCCAGGAGGAGTGTCCCTG 1840

RESULT 4

US-09-949-016-748
 ; Sequence 748, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 748
 ; LENGTH: 4163
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-748

Query Match 3.1%; Score 62; DB 3; Length 4163;
 Best Local Similarity 47.2%; Pred. No. 2.9e-05;
 Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;
 1463 GTCTGTGGGAGCACTGGCGTGTGAGCCAGATGCCACTGGCGGTGGCGCTGGGAC 1522
 1527 GCGTGGAGTGGCCACCGGGCGCTTGGAGGCGCTGGAGGCTTCTTGGAGGTCTGGCAC 1586
 1523 TGTGGAGCGCGCGAGCTGAGCGCGCAGCGAGCCTAGCTGCTTCCACACAGCGAC 1582
 1587 TGCAGGGCAACCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1646
 1583 GCGGTATCTGACGAGGGTGGGTGATCTTCTTCTGCGCCGCGCGCTGGCGC 1642
 1647 GCGTCAATCTTGGCGAGAACCGCCTGAGCCACTTCCCGCTGGACACAGGCTGTGTAC 1706
 1643 AGTGTGACGAGTGGCTGAGCTCCAGACAGTGGAGCCCGGGCGCATGACGCCCTGGCG 1702
 1707 TGGAGTGTGGACCTTGGGAACACAGCTTCCAGCTTCTGCGAGGAGTGCATGGGTG 1766
 1703 CTTGGCTCAGCTGCTGCTACCGGATTTCTTGCAGAGCGCGGGGACCGCGCTAGCTG 1762
 1767 GCGTGGAGACCAAGCCTCCGCGCTTACTCTGAGGGGAATCCACTCAGCTGCTGGGCA 1826
 1763 GGTGTACTTTCAGCGGCTGCTGACCCAGACTCTGTGCGCTTCCCGGTTCGCGTGGCC 1822

Db 1827 ATGGCTGGCTGGCAGCCAGCTGCACCAAGGCGCTGTGGAGCTGGAGCCACCCAGGACC 1886
Qy 1823 CGCTCTTCTCCCTCCCAAGCAGCTGCGCGCTTTCCTG 1860
Db 1887 TGATCTGCGCTTCAGCTCCCAAGGAGGAGTGTCCCTG 1924

RESULT 5
US-09-949-016-16581
; Sequence 16581, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16581
; LENGTH: 12438
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16581

Query Match 3.1%; Score 62; DB 3; Length 12438;
Best Local Similarity 47.2%; Pred. No. 4.2e-05;
Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

Qy 1463 GTCTGGTGGGAGCACTGGCTCCGCTTGAGCCAGATGCCACTGCGGCTGGGCGTGGACC 1522
Db 7805 GGCTGGAGGTGGCCACGCGGGCCCTTGGAGGCCCTCTCTGGAGGTCTCTGGCAC 7864
Qy 1523 TGTGGAGCGCGGAGCTGAGCGCGCAGCGAGCCCTAGCTGTCTCCACACCCAGCGAC 1582
Db 7865 TGCAGGGCAAGGGCTCATGTCTCTGAGGTGACCTGCGCTGCTTATCTGCTCAAGC 7924
Qy 1583 GCGTATCTCTGAGAGGGTGGGTGTATCTCTTCTCTGCGCGCGCGCTGGCGC 1642
Db 7925 GGCTCAATCTTGGCGAGAACCGCTGAGCCACCTTCCGCTGAGACAGGCTGTGCAC 7984
Qy 1643 AGTGTACAGAGTGGCTGAGCTCCAGACAGTGGAGCGCGCGCGCATGACGCCCTGCGC 1702
Db 7985 TGGAGGTGTGGACCTGCGAAACACAGCTTTCAGCTCTCTGCCAGGCGAGTGCCATGGGTG 8044
Qy 1703 CTGGCTCAGTGGCTACCGGATTTCTGCAAGCGCGGCGGAGCCGCTAGCTCG 1762
Db 8045 GCCTGGAGACAGGCTCCGGCGCTTACCTGCAAGGGAATCCACTGAGCTGTGGCGCA 8104
Qy 1763 GGGTCTACTTTCAGCGGCTGTGCACCCAGACTGTGTCCTCCCTCCCGTTCGGGTGCGCC 1822
Db 8105 ATGGCTGGCTGGCAGCCAGCTGCACCAAGGCGCTGTGGAGCTGGAGCCACCCAGGACC 8164

Qy 1823 CGCTCTTCTCCCTCCCAAGCAGCTGCGCGCTTTCCTG 1860
Db 8165 TGATCTGCGCTTCAGCTCCCAAGGAGGAGTGTCCCTG 8202

RESULT 6
US-09-949-016-12490
; Sequence 12490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12490
; LENGTH: 16321
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)-(16321)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12490

Query Match 3.1%; Score 62; DB 3; Length 16321;
Best Local Similarity 47.2%; Pred. No. 4.6e-05;
Matches 188; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

Qy 1463 GTCTGGTGGGAGCACTGGCGTCCGCTTGAGCCAGATGCCACTGCGGCTGGGCGTGGACC 1522
Db 11692 GGCTGGAGGTGGCCACGCGGGCCCTTGGAGGCCCTCTTGGAGGTCTCTGGCAC 11751
Qy 1523 TGTGGAGCGCGCGAGCTGAGCGCGCAGCGAGCCCTAGCTGTCTCCACACCCAGCGAC 1582
Db 11752 TGAGGGCAAGGGCTGATGTCTCTGAGGTGACCTGCCGCTTCATCTGCTCAAGC 11811
Qy 1583 GCGTATCTCTGAGGAGGTGGCGTGTATCTCTTCTGCGCGCGCGCTGGCGC 1642
Db 11812 GGCTCAATCTTGGCGAGAACCGCTTGAGCCACCTTCCGCTTGGACACAGGCTGTGCAC 11871
Qy 1643 AGTGTACAGAGTGGCTGAGCTCCAGACAGTGGAGCGCGCGCGCATGACGCCCTGCGC 1702
Db 11872 TGGAGGTGTGGACCTGCGAAACACAGCTTTCAGCTCTCTGCCAGGAGTGGCATGGGTG 11931
Qy 1703 CTGGCTCAGTGGCTGCTACCGATTTCTGCAAGCGCGCGCGAGCCGCTAGCTCG 1762
Db 11932 GCTGGAGACCAAGCTTCCGGCGCTCTACTGCAAGGGAATCACTGAGCTGTGGCGCA 11991
Qy 1763 GGGTCTACTTTCAGCGGCTGCTGCACCCAGACTGTGTGCTTCCCGTTCGCGTGGCGC 1822
Db 11992 ATGGCTGGCTGGCAGCCAGCTGCACCAAGGCGGTGTGGAGCTGGAGCCACCCAGGACC 12051
Qy 1823 CGCTCTTCTCCCTCCCAAGCAGCTGCGCGCTTTCCTG 1860
Db 12052 TGATCTGCGCTTCAGCTCCCAAGGAGGAGTGTCCCTG 12089

RESULT 7
US-09-902-540-934
; Sequence 934, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 934
; LENGTH: 7950
; TYPE: DNA

Thu Aug 17 14:34:40 2006

ORGANISM: Myxococcus xanthus

US-09-902-540-934

Query Match 2.7%; Score 54; DB 3; Length 7950;
Best Local Similarity 44.7%; Pred. No. 0.0034;
Matches 253; Conservative 0; Mismatches 310; Indels 3; Gaps 1;

QY 1427 TGCTCTCCACTCCGCGCGAGCGGGCTACAGAGCGTGTGGTGGAGCACTGGCGTCCG 1486
DB 2807 TGGCCAGCACCTGCATGACGAGCGCTCCACGTCGCGCAGCTAAACGGCGCACTGCGGT 2866
QY 1487 GCTTGAAGCAGATGCCACTGCGGTGGCGGACCTGTGGAGCGCGGAGCTGAGCG 1546
DB 2867 CGGTCTCCGCGAGCAGAAAGATGGGGTAGCCACAGTTGGCGGGCCATGTTAGTG 2926
QY 1547 GCGACGAGCCCTAGCTGTGTTCCACACGAGCGCGGTATCTCGAGGAGGGTGGCG 1606
DB 2927 AGCTGCGGCCAGGTTGGTCTCGAAGACCTCGCGCCCTCTTCGCCAATCGCGGTG 2986
QY 1607 TGGTAATCTTCTTCTCGCGCGCGGTGGCGGAGTGTGAGTGGCTGAGCTCC 1666
DB 2987 CTGGCAGCATGTTCTACGCTTCGCGGACCGGCCAGGTGAGATGGCGGGTGTCTC 3046
QY 1667 AGACAGTGAGCGCGCGCGCATGACGCGCTCGCGCCCTGCGCGCGCATCTCGCTGAAGAGGTGCATC 3106
DB 3047 AGAGAGCAGCAGCATCGCGGAGAGCCCTCGCGCGCATCTCGCTGAAGAGGTGCATC 3106
QY 1727 ATTTCCTGCAAGCGCGGGCGACGCGCGCTAGCTGGGGTCTACTTCGACGGGCTGTGC 1786
DB 3107 AGCGGAGCGCGCTCTCGTACTCACTCGCGCCAGCGGTGACACGGTATGTTGTCATG 3166
QY 1787 ACCAGACTGTGCGCTTCCCGTTCGCGGTGCGCGCTCTTCTTCCCTGCGCGCGAGC 1846
DB 3167 ACCTGCTCTTCTTCTGAGCC--TTTCGCGTGGCGAGGGCTTACGCTGGCGCGCAGGC 3223
QY 1847 TGCGCGCTTCTCTGATGCACTGAGGAGGCTGCTCACTTCGCGGGCGCGACCGCGG 1906
DB 3224 TCCAGGTTCCCGTGGGTACCGGTTGAGGAGGCGATGCACTGCGCGCGCGCGCGG 3283
QY 1907 ACCGGTGGACGAGTACCGCGCGCTGCGGTGCGCGCTGCGCGCGCGCGCGCGG 1966
DB 3284 AGCGGCTGGCTCTCTGGCGCAGCGCCATGACACTTCTTCGGAGACGCGAGACCGCGGCT 3343
QY 1967 CGGAAGCGCCAGGCTGCTGCGAGAA 1992
DB 3344 CTCGCGAGCGCAGGCGCTGGCGGCA 3369

RESULT 8

US-10-324-967-31

Sequence 31, Application US/10324967

Patent No. 6974680

GENERAL INFORMATION:

APPLICANT: Cosson, Pierre

APPLICANT: Kohler, Thilo

APPLICANT: Benghezal, Mohammed

APPLICANT: Marchetti, Anna

APPLICANT: van Deiden, Christian

TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE

FILE REFERENCE: 25421-502

CURRENT APPLICATION NUMBER: US/10/324,967

CURRENT FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patent in version 3.2

SEQ ID NO 31

LENGTH: 5430

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-10-324-967-31

Query Match 2.5%; Score 51.4; DB 4; Length 5430;

Best Local Similarity 47.1%; Pred. No. 0.013;

Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 1546 GCGCACGAGCCCTAGCTGTTCCACACGAGCGCGGTATCTCTGAGAGGGTGGC 1605
DB 3436 GCCATCGCGCCATCTGTCGAGCGCCGCAACGCGGCTGGCGCTTGGCTTGGC 3495
QY 1606 GTGGTAATCTTCTTCTTCTGCGCGCGCGTGTGCGAGTGTCTGAGAGCTTGGC 1665
DB 3496 GCGCGCACCGCGCGCGCGCGAGCGCGATCGCCGGTGGCGCGCTGCTGAGCGA 3555
QY 1666 CAGACAGTGGAGCGCGCGCGCGATGACGCCCTCGCGCGCTGCTCAGCTGCTATCCC 1725
DB 3556 GCGCGGAGGTGACTACTCTGTTACCGACGTTTCCAGCTACTTCTCGCGCGCGCGC 3615
QY 1726 GATTTCTCTCAAGCGCGCGCGCGCGCTACGTCGCGGCTCTACTTCGACGGGCTGTG 1785
DB 3616 GAGCGCTTCGCGCGAGCAGCGCGGTGGTACGCTTCGCGCGCTTCGACATGAACGGGATCTT 3675
QY 1786 CACCAGACTCTGTGCGCTTCCCGCTTCGCGGTGCGCGCGCTTCTCTCCCTGCCACGAG 1845
DB 3676 CTCGACGAGCGGTGGCGCGCGCTCGGTGATATCTCTGCTAGCTCCGCGGCTTGAAC 3735
QY 1846 CTCGCGCTTCTGATGATGCACTGCGAGGAGC 1878
DB 3736 AACCGCTGACACACCGCGCGCTGCTGCGCGC 3768

RESULT 9

US-10-012-231A-259/c

Sequence 259, Application US/10012231A

Patent No. 6924355

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2830P1C23

CURRENT APPLICATION NUMBER: US/10/012,231A

CURRENT FILING DATE: 2002-06-10

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 477

SEQ ID NO 259

LENGTH: 4563

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

LOCATION: 3635

OTHER INFORMATION: unknown base

US-10-012-231A-259

Query Match 2.5%; Score 50; DB 3; Length 4563;

Best Local Similarity 45.5%; Pred. No. 0.027;

Matches 214; Conservative 0; Mismatches 255; Indels 1; Gaps 1;

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DB 485 CGCGCGGTCTCCCG 426

QY 1463 GTCTGGTGGAGC-ACTGGCGTCCCGGTTGAGCAGATGCCACTGCGCTGCGGTGGAC 1521

DB 425 GCGCTCAGCGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366

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Db	425	GCCCTCAGCCCGTGGCCCCCGCCACCGAGAGCCACGCCGCCCTTAGCGCCGCGAGGCGCCCG	366		

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[illegible]

RESULT 13
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; Sequence 259, Application US/10015393A
; Patent No. 6951737
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477

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Db	305	GCAGGCCCCGCGCGCGCTTTTTCGCAACACCGCCGCCCGCGCGGCTTCGCCT	246	
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Db	245	TTAGAGGGGACCATGCGCGCGCTAGCGCGGCTCGGCGCGCAGGTGGCGCGGC	186	
QY	1702	GCCTGGCTCAGCTCGGTGCTACCGGATTTCTGCAAGCGCGGCGACCGGCGGTACGTC	1761	
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RESULT 12
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; Sequence 259, Application US/10015671A
; Patent No. 6946263
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015, 671A
; CURRENT FILING DATE: 2001-12-11
; prior application removed - See File Wrapper or Palm

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[illegible]

Thu Aug 17 14:34:40 2006

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QY	1822	CCGCTCTTCTCCCTGCCACGCGAGCTGCCGCTTTCTTGGATGCACTGCA	1871
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Search completed: August 16, 2006, 23:58:07
Job time : 395 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 09:07:13 ; Search time 2082 Seconds
(without alignments)
5966.762 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3605	100.0	2256	8	US-10-719-202-1	Sequence 1, Appli
3	3583	99.4	2328	3	US-09-899-471-4	Sequence 4, Appli
4	3583	99.4	2328	8	US-10-719-202-4	Sequence 4, Appli
5	3572.5	99.1	2269	16	US-11-150-533-25	Sequence 25, Appli
6	3569.5	99.0	2287	16	US-11-150-533-29	Sequence 29, Appli
7	3565	98.9	2314	3	US-09-863-618A-7	Sequence 7, Appli
8	3565	98.9	2314	9	US-10-749-144-7	Sequence 7, Appli
9	3565	98.9	2314	9	US-10-924-667-7	Sequence 7, Appli
10	3562	98.8	2128	3	US-09-866-050A-487	Sequence 487, App
11	3562	98.8	2128	3	US-10-152-661-487	Sequence 487, App
12	3539	98.2	2331	8	US-10-416-442A-74	Sequence 74, Appli
13	2666	74.0	2022	3	US-09-899-471-3	Sequence 3, Appli
14	2666	74.0	2022	8	US-10-719-202-3	Sequence 3, Appli
15	2644	73.3	2094	3	US-09-899-471-6	Sequence 6, Appli
16	2644	73.3	2094	8	US-10-719-202-6	Sequence 6, Appli
17	2352.5	65.3	2255	7	US-10-458-647-1	Sequence 1, Appli
18	2352.5	65.3	2255	16	US-11-150-533-1	Sequence 1, Appli
19	2339	64.9	2380	3	US-09-874-503-13	Sequence 13, Appli
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21	2339	64.9	2380	3	US-09-808-827-13	Sequence 13, Appli
22	2339	64.9	2380	6	US-10-006-867-161	Sequence 161, App
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45	2339	64.9	2380	6	US-10-176-913-597	Sequence 597, App

ALIGNMENTS

RESULT 1

US-09-899-471-1
; Sequence 1, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197) ... (2218)
US-09-899-471-1

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Best Local Similarity: 100.0%
Query Match: 100.0%
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Gaps: 0
Indels: 0
Mismatches: 0

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; Sequence 1, Application US/10719202
; Publication No. US20040121388A1

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US-10-719-202-1

; Sequence 1, Application US/10711

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; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197) ... (2218)
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Score: 3605.00 Matches: 674
Percent Similarity: 100.0% Conservative: 0
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Tue Aug 22 11:34:35 2006

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1937 CCGGCGACCGGCGCTAGCTGGGGTCTACTTCACCGGGTGTGACCCAGACTCTGTG 1996
QY
601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
DB
1997 CCTCCCGGTTCCGGGTCGCCCGCTCTCTCTCCCTGCCCCACGACGCTGCGGGCTTCTCG 2056
QY
621 AspAlaLeuGlnGlyCysSerThrSerThrSerThrSerThrSerThrSerThrSerThr 640
DB
2057 GATGCACTGCAGGAGGCTGCTCCACTTCGCGGGGCGACCCGCGGACCGGGTGGAAACGA 2116
QY
641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
DB
2117 GTGACCCAGGCGCTCGGGTCGCCCTCGACAGCTGTACTTCTAGCTCGGAAGCCCGAGGC 2176
QY
661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
DB
2177 TGCTGGAGGATGGACCTGGGACCTGCACACTAGAA 2218

RESULT 3
US-09-899-471-4
; Sequence 4, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197) ... (2290)
US-09-899-471-4

Alignment Scores:
Pred. No.: 0 Length: 2328
Score: 3583.00 Matches: 674
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 0
Query Match: 99.4% Indels: 24
DB: 3 Gaps: 1

US-10-719-202-2 (1-674) x US-09-899-471-4 (1-2328)
QY
1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
DB
197 ATGCTGTGTCTCGTTCCTGCTCTGCTTGGCACTGGGCGGAAACCCCTGGTGGTCTCT 256
QY
21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB
257 CTGGAGAGACTGATGGAGCCCTCAGACACTGCACGCTGCTCTTAGGCGCTCTCTCGCCAC 316
QY
41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB
317 CTCTGGGATGTGACGTCTCTGCTGCTGGAGCCCTCCAGTCTGCGCCCGGCGCTGTG 376
QY
61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB
377 CTAGTGCCTACCCGCTCGACGCGAGCTGGTGTGCTGAGGTGTCCACAGACAGATTGC 436
QY
81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB
437 GCCCTCCGGTCCGTTGGTGTGTCCACTTGGCGTGCATGGGCCTGGGCGAGAGCTGAA 496
QY
101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
DB
497 GAAGCTGGAAAGTCTGATTGATTGAGAGTCTCAGAAAGCGCTCTCTCCAGGCCCGNG 556

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121 ValValLeuSerPheGlnAlaTrpProLeuAlaArgCysAlaLeuLeuGluValGlnVal 140
DB
557 GTGGTGTCTCTCTCCAGGCTTACCCATCGCCGCTGTGCTCCCTGGAGGTCCAGGTG 616
QY
141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB
617 CCCGCTGACCTCGGTGAGCTGTGCTCAGTCCGTTGGGTCTTGGGTATTGACTGTTCGAG 676
QY
161 AlaSerLeuGlyAlaGluValGlnLeuTrpSerTrpThrLysProArgTrpGlnLysGlu 180
DB
677 GCTAGTCTTGGGCTGAGGTACAGATCTGGTCTCAGAGCCCGAGGTACAGAAAGAG 736
QY
181 LeuAsnLeuThrGlnGlnLeuPro----- 188
DB
737 CTCACCTCACAGCAGCTGCTGACTCAGGGGTCTTGAAGTCCGGGACAGCATCCAG 796
QY
189 -----AspGlyAspAsnValLeuLeuThr 196
DB
797 AGCTGTGGGTCTCGCCCTGGCTCAATGTGTCTACAGATGGTGACAATGTCTTCTGACA 856
QY
197 LeuAspValSerGluGlnGlnAspPheSerPheLeuLeuTrpLeuArgProValProAsp 216
DB
857 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACTCTGCTCCAGTCCCGGAT 916
QY
217 AlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsnLeuThrLeuAsnHis 236
DB
917 GCTCTCAATCTTGTGTGTTACAAACCTGACTGGACCTCAGAACATTACTTTAAACCCAC 976
QY
237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
DB
977 ACAGACTGGTTCCTCGCTCTGCAATTCAGTGTGGTGGTGTAGAGCCAGACTCTGAGAGG 1036
QY
257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
DB
1037 GTCGAATTCGCCCCCTTCGCGGAGATCCCGGTGCACACAGGAACCTCTGGCACATAGCC 1096
QY
277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
DB
1097 AGGCTGGGGTACTGTCTCCAGGGGTATGGCAGCTAGATGGCTTGTGTCTCCGGGC 1156
QY
297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
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1157 AAGGTAAACACTGTGCTGGCAGGACCCAGACCCAGAGTCCCTGCCAGCCACTTGTGCCACCA 1216
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317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
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1217 GTGCCCCAGAGAGACGCCACTGTGAATGAGCCACCAAGATTTCCAGTTGGTGGCAGGCCAC 1276
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337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
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1277 CCCAACCTCTGTGTCCAGGTGAGCACCTGGGAGAGAGTTTCAAGTGTGCAAGCGTCTCGTGG 1336
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357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
DB
1337 GCTGACTCTCTGGGGCCCTTCAAGGATGATGTGTGTAGTGGAGATGAAAACCGGCTC 1396
QY
377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
DB
1397 AACCAACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1456
QY
397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
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1457 TCCACGAGAGCTGCTCGCTTGGGAGGAGGTGTGCTGCAAGACTTCCGATCACACCATGT 1516
QY
417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrp 436
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1517 ATGACGCTGTGGAAACGATGACAACATGGGATCGCTATGGGCTTGGCCCATGGCAAGTAC 1576
QY
437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaLeuPhe 456
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1577 ATCCACAGGCGCTGGGTCTTAGTATGGCTGGCCCTGCTACTCTTGGTGGGCGCTTTTC 1636

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1217 GTGCCCCAGAAAGCCACCTGTGATGAGCCACACAGATTTCAGTTTGGTGGCAGGCCAC 1276
337 ProAenLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
1277 CCCAACCTCTGTCTCAGCTGAGCACCCTGGGAGAGGTTTCAGCTGCAGCGTGTCTGTGG 1336
357 AlaAapSerLeuGlyProPheIysAspMetLeuLeuValGluMetLysThrGlyLeu 376
1337 GCTGACTCTTGGGGCCCTTCAAGATGATATGCTTGTAGTGGAGATGAACACCGGCTC 1396
377 AenAenThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
1397 AACACACATCAGTCTGTGCTTGGACCCAGTGGCTGTACACACATGCCCCAGCATGGCC 1456
397 SerThrArgAlaAlaArgLeuGlyClnGluLeuGlnAlaPheArgSerHisGlnCys 416
1457 TCCACGAGAGCTGCTCGCTGGGAGAGAGTGTGTCAGAGACTTCCGATCACACAGTGT 1516
417 MetGlnLeuTrpAsnAspAspMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
1517 ATGCAGCTGTGAAACATGACACATGGATGGATCGCTATGGGCTGCCCATGGACAGTAC 1576
437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
1577 ATCCACAGCGCTGGTCTCTAGTATGGCTGGCTGCTACTCTTGGCTGGCGGCTTTTC 1636
457 PhePheLeuLeuLeuLysIysAspArgLysAlaAlaArgGlySerArgThrAlaLeu 476
1637 TTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1696
477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
1697 CTCCTTCACTCCGCCGAGAGCGGCTAGGAGCGTCTGGTGGAGCACTGGCGTCCGCG 1756
497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgLeuLeuSerAla 516
1757 TTGAGCCAGATGCATCGGCGTGGCGTGGACCTGTGGAGCGCGCGGAGCTGAGCGG 1816
517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlyGlyVal 536
1817 CAGGAGCCCTAGCTGTGTTCACACACAGCGGCGGCTATCTGACGAGGGTGGCGTG 1876
537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeu 556
1877 GTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1936
557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
1937 ACAGTGGAGCCCGGCGCATGACGCCCTCGCCGCTGGCTAGCTGCGTGTACCCGAT 1996
577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTrpPheAspGlyLeuLeuHis 596
1997 TTCTTGCAGCGCGGCGCACCGGCGCTACGTGGGGTCTTACTTCGACGGGCTGTGCAC 2056
597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
2057 CCAGACTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2116
617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
2117 CCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2176
637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
2177 CCGGTGGACGAGTGCACCGGCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 2236
657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
2237 GAAGCCCGAGGCTGCTCGAGGAATGGACCTGGGACCTTGCATCTACACTAGAA 2290

Sequence 25, Application US/11150533
Publication No. US20060002925A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Burkhead, Steven K.
APPLICANT: Levin, Steven D.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
APPLICANT: Jaspers, Stephen R.
APPLICANT: Bilsborough, Janine
TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
TITLE OF INVENTION: INFLAMMATION
FILE REFERENCE: 04-06P1
CURRENT APPLICATION NUMBER: US/11/150,533
CURRENT FILING DATE: 2005-06-10
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 2269
TYPE: DNA
ORGANISM: Mus musculus
US-11-150-533-25
Alignment Scores:
Pred. No.: 0 Length: 2269
Score: 3572.50 Matches: 671
Percent Similarity: 98.4% Conservative: 1
Best Local Similarity: 98.2% Mismatches: 2
Query Match: 99.1% Indels: 9
Gaps: 16
DB:

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Db 197 ATGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 256
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 257 CTGGAGAGACTGTATGGAGCCCTCAGGACACTGCACGCTGCTCTCTAGGCTCTCTCT 316
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 317 CTCTGGATGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 376
Qy 61 LeuValProThrArgLeuGlnThrClnLeuValLeuArgCysProGlnLysThrAspCys 80
Db 377 CTAGTGCCTACCGGCTGCAGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 436
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 437 GCCCTCTGTGTCTGT 496
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnSerArgAsnAlaSerLeuGlnAlaGln 120
Db 497 GAAGCTGGAAGTCTGATTCAGAACTCCAGGAGTCTAGGAGCGCTCTCTCCAGGCCAG 556
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 557 GTGGTGTCTCTCTTCCAGGCTTACCCCATCGCCCGCTGTGTGTGTGTGTGTGTGTGT 616
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 617 CCGCTGACCTGTGTGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 676
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 677 GCTAGTCTTTGGGCTGAGGTACAGATCTGTCTCTACAGAGCCCGGCTGTGTGTGTGT 736
Qy 181 LeuAsnLeuThrGlnGlnLeuPro-----AspGlyAsp 191
Db 737 CTCACCTCACACAGGAGCTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 796

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QY 192 AsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeu 211
DB 797 AATGTCCTCTCGACACTGGATGCTCTCGAGGAGCAGGACTTTAGCTTCTTACTGTACCTG 856
QY 212 ArgProValProAspAlaLeuLysSerLeuTyrTrpLysAsnLeuThrGlyProGlnAsn 231
DB 857 CGTCCAGTCCCGGATGCTCTCAATCCCTTGTGGTACAAAACCTGACTGACCTCAGAAC 916
QY 232 IleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGlu 251
DB 917 ATTACTTTAAACCAACAGACCTGGTTCCCTGCTCTGCAATTGAGGTGTGCTCGCTAGAG 976
QY 252 ProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 271
DB 977 CCAGACTCTGAGAGGGTCAATTCGCCCCCTCCCGGGAAGATCCCGGTGCACACAGGAAC 1036
QY 272 LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaPro 291
DB 1037 CTCTGGCACATAGCCAGGCTGCGGGTACTGTGCCCCAGGGGTATGGCAGCTAGATGCGCCT 1096
QY 292 CysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGln 311
DB 1097 TGTCTGCTCCGGGCAAGGTAACTGTCTGGCAGGCAACACAGCAGAGTCCCTGCGCAG 1156
QY 312 ProLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGln 331
DB 1157 CCACCTTGTGCCACAGTGGCCCCAGAGAACGCCACTGTGAATGAGCCACAGATTTCCAG 1216
QY 332 LeuValAlaGlyHisProLeuLeuCysValGlnValSerThrTrpGluLysValGlnLeu 351
DB 1217 TTGGTGGCAGGCCACCCCAACCTCTGTGTCCAGGTGAGCACCCTGGGAGAAGGTTACAGTCG 1276
QY 352 GlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGlu 371
DB 1277 CAAGCGTGTGTGGGGTGACTCCTTGGGGGCCCTTCAAGGATGATATGCTGTAGTGGAG 1336
QY 372 MetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrPro 391
DB 1337 ATGAAAACCGGCTCAACACACATCAGTCTGTGGCTTGGNACCCAGTGGCTGTACACCA 1396
QY 392 LeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPhe 411
DB 1397 CTGCCCAGATGGCCTCCACGAGAGCTGCTCGCCTGGGAGAGTTGCTGCAAGACTTC 1456
QY 412 ArgSerHisGlnCysMetGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCys 431
DB 1457 CGATCACACAGGTATGCAAGCTGTGGNACGATGACAAACATGGGATCGCTATGGGCTGC 1516
QY 432 ProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeu 451
DB 1517 CCATGTGACAGTACATCCACAGCGCTGGGTCTGTAGTATGGCTGGCTGCTTCTTGTG 1576
QY 452 AlaAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGly 471
DB 1577 GCTGCGCGCTTTTCTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1636
QY 472 SerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGly 491
DB 1637 TCCCGCACCGCCCTTGTCTCTCCACTCCGCGCAGCGGCTGACGAGCGTCTGTGGTGGGA 1696
QY 492 AlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArg 511
DB 1697 GCATGTGGGTCCCGTTGACAGATGCCACTGCGGTGGCCGTGGACCTGTGGAGCCGC 1756
QY 512 ArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgGlyLeu 531
DB 1757 CGCGAGCTGAGCGCGCAGCGAGCCCTAGCTGTGTCCACCCAGCAGCGCGGTATCCTG 1816
QY 532 GlnGluGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGln 551
DB 1817 CAGGAGGTGGGTGTAATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1876
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DB 1877 TGGCTCAGCTCCAGACAGTGGAGCCGCGCATGAGCCCTCGCGCTGGCTCAGC 1936
QY 572 CysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPhe 591
DB 1937 TGGCTGCTACCCGATTTCTGCAAGGCCGCGGCGCATGCGCGCTACGTGCGGGTCTACTTC 1996
QY 592 AspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSer 611
DB 1997 GACGGGCTGCTGCACCCAGACTCTGTGCGCTTCCCGTTCGCGCTGCGCGCTCTTCTCC 2056
QY 612 LeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAla 631
DB 2057 CTGCCCTCGCAGCTGCGCGCTTCTTCTGATGCACCTGACGAGGAGGCTGCTCCTCCTCCGCG 2116
QY 632 GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSer 651
DB 2117 GGGCGACCCCGCGACCCGGGTGGAAACGAGTGACCCAGCGCTGCGGTCCGCGCTGGACAGC 2176
QY 652 CysThrSerSerSerGluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThr 671
DB 2177 TGTACTTCTAGCTCGGAGCCCGAGGCTGCTGCGAGGATGGGACCTGGGACCTGGACCT 2236
QY 672 ThrLeuGlu 674
DB 2237 ACACTAGAA 2245
RESULT 6
US-11-150-533-29
; Sequence 29, Application US/11150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-150-533-29
Alignment Scores:
Pred. No.: 0 Length: 2287
Score: 3569.50 Matches: 671
Percent Similarity: 97.5% Conservatives: 1
Best Local Similarity: 97.4% Mismatches: 2
Query Match: 99.0% Indels: 15
DB: 16 Gaps: 1
US-10-719-202-2 (1-674) x US-11-150-533-29 (1-2287)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
DB 197 ATGCTGTGTCTCTGTTCTCTGCTGCTTGGCAGCTGGGCGGAAACCTGTGGTGGTCTCT 256
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 257 CTGGAGAGACTGATGGAGCTCAGGACACTGACGCTGCTCTCTAGGCTCTCTCTGCTCCAC 316
QY 41 LeuTrpAspGlyAspValLeuLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
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; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (199)..(2292)
; OTHER INFORMATION:
; NAME/KEY: mat peptide
; LOCATION: (259)..()
; OTHER INFORMATION:
US-09-863-818A-7

Alignment Scores:
Pred. No.: 0 Length: 2314
Score: 3565.00 Matches: 671
Percent Similarity: 96.3% Conservative: 1
Best Local Similarity: 96.1% Mismatches: 2
Query Match: 98.9% Indels: 24
DB: 3 Gaps: 1

US-10-719-202-2 (1-674) x US-09-863-818A-7 (1-2314)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
DB 199 ATGCCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 259 CTGGAGAGACTGATGAGAGCTTACGACATGACAGCTGCTCTCTAGGCTCTCTGCCAC 318
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 319 CTCTGGAGTGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB 379 CTAGTGCCTACCGCTGACGAGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438
QY 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB 439 GCCCTCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
DB 499 GAAGCTGGAAGTCTGATTCAGAACTCCAGAGTCTTAGGAGCTCTAGGAGCTCCAG 558
QY 121 ValValLeuSerPheGlnLafyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
DB 559 GTGGTGTCTCTCTCCAGGCTACCCCATCGCCGCTGTGTGTGTGTGTGTGTGTGTGT 618
QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB 619 CCGCTGTGACTGTGTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 678
QY 161 AlaserLeuGlyAlaGluValGlnIleTrpSerFyrThrLysProArgTyrGlnLysGlu 180
DB 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGTGTCTTACAGAGCCAGGTACCAAGAG 738
QY 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
DB 739 CTCAACCTCACAAGCAGCTGCTGTGCTGAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
QY 189 -----AspGlyAspAsnValLeuLeuThr 196
DB 799 AGCTGTGGGTCTGCGCTTCAATGTGTCTACAGATGTGTACAAATGTCTTGTGACA 858
QY 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTrpLeuArgProValProAsp 216
DB 859 CTGGATGTCTCTGAGGAGCAGGACTTGTAGTCTTACTGTACCTGTGTGTGTGTGTGT 918
QY 217 AlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
DB 919 GCTCTCAAAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 978
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QY 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
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QY 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
DB 1039 GTCGAATTCTGCCCTTCCGGGAAGATCCGGGTGCAACACAGGAACTCTGGCACA 1098
QY 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
DB 1099 AGGCTCGGGGTACTGTCCCGAGGGGTATGACAGTATGCGCTTGTGTCTGCGGGC 1158
QY 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
DB 1159 AAGGTAACTGTGCTGGCAGGCACACAGAGTCCCTGCTGCTGCTGCTGCTGCTGCT 1218
QY 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
DB 1219 GTGCCCCAGAGAAACGCCACTGTGTAATGAGCACAAGATTTCAGTTGGTGGCAGCC 1278
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLeuValGlnLeuGlnAlaCysSerTrp 356
DB 1279 CCAACCTCTGTGTCCAGGTGAGCACCTGGAGAGAGGTTCAGCTGCAAGCGTCTGTGG 1338
QY 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
DB 1339 GCTGACTCTTGGGGCTTCAAGGATGATATGCTGTGTAGTGAGATGAAACCGGCTC 1398
QY 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
DB 1399 AACAAACATCATGCTGTGCTTGGAAACCCAGTGGCTGTACACACTGCCAGCATGGCC 1458
QY 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
DB 1459 TCACAGAGAGTGTCTGCTGGAGAGAGTGTCTGCAAGACTTCCGATCACACAGTGT 1518
QY 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrp 436
DB 1519 ATGCAGCTGTGNAACGATGACACATGGATGCTATGGGCTGCTGCTGCTGCTGCTG 1578
QY 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
DB 1579 ATCCACAGCGCTGGTCTCTAGTATGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 1638
QY 457 PhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu 476
DB 1639 TTCTTCTCTCTTCTTAAAGAGACCGCAGGAAAGCGGCTGCTGCTGCTGCTGCTGCT 1698
QY 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
DB 1699 CTCCTCCATCTCGCCGACGAGCGGGCTACGAGCGCTGCTGAGGACACTGGGCTCGCG 1758
QY 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAla 516
DB 1759 TTGAGCCAGATGCCACTGCGCTGGCGGTGGACCTGTGTGAGCGCGCGCGAGCTGAG 1818
QY 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlyGlyVal 536
DB 1819 CACGAGCGCTAGCTGTGTTCCACCAACCGCAGCGCTATCTCTGAGGAGGGTGGCGTG 1878
QY 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
DB 1879 GTAATCTTCTCTTCTGCGCCCGCGCGGTGGCGCGAGTGTGAGCAGTGGCTGAGCTCC 1938
QY 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
DB 1939 ACAGTGGAGCGCGGGCGCATGACGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998
QY 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
DB 1999 TTCTCTCAAGGCGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2058
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QY 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
DB 2059 CCAGACTCTGTGCCCTCCCGTTCGGCTCGCCCGCTCTTCTCCCTCCCTCGCAGCTG 2118
QY 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
DB 2119 CCGGCTTTCCTGGATGCACTGCAGGAGGCTGCTCATTCCGGGGGGGACCCGGGAC 2178
QY 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
DB 2179 CGGGTGGAAACAGTGCACCCAGGCGCTGGCTCCGCCCTGGACAGCTGTACTTCTAGCTCG 2238
QY 657 GluAlaProGlyCysGluGluThrPheLeuGlyProCysThrThrLeuGlu 674
DB 2239 GAAGCCCCCAGGCTGCTGGAGGAATGGGACCTGGGACCCCTGCACCTACACTAGAA 2292

RESULT 8
US-10-749-144-7
; Sequence 7, Application US/10749144
; Publication NO. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(2292)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (259)..()
US-10-749-144-7

Alignment Scores:
Pred. No.: 0 Length: 2314
Score: 3565.00 Matches: 671
Percent Similarity: 96.3% Conservatives: 1
Best Local Similarity: 96.1% Mismatches: 2
Query Match: 98.9% Indels: 24
DB: 9 Gaps: 1

US-10-719-202-2 (1-674) x US-10-749-144-7 (1-2314)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
DB 199 ATGCCTGTGTCTGTCTCTGCTCTGCTCTGGCAGCTGGCGCGAAACCTGTGGTGTCTCT 258
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
DB 259 CTGGAGAGACTGATGAGGCTCAGGACATGACACGCTGCTCTCTAGGCTCTCTCTGCCAC 318
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
DB 319 CTCTGGGATGGTACCTGTCTCTGCTCTGCTGGAGGCTCCAGTCTGCCCGCCAGGCCCTGTG 378
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
DB 379 CTAGTGCCTACCCGCTGCAGAGGAGCTGCTGAGGTGTCCACAGAAACAGATTGC 438
QY 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
DB 439 GCCCTCTGTCTCGTGTGGTGGTCCACTTGGCCGTGCATGGGACCTGGCGCAGAGCCCTGAA 498
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
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DB 499 GAAGCTGGAAAGTCTGATTCCAGAACTCCAGGAGCTAGGAAGCGCTCTCTCCAGGCCAG 558
QY 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
DB 559 GTGGTGTCTCTCTCCAGGCGCTACCCCATCCGCCGCTGTGCCCTGCTGGAGGTCCAGGTG 618
QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
DB 619 CCCGCTGACCTGTGGTGGAGCCCTGGTCACTCCGTGGGTCTCGGGTATTGTGACTGTTCGAG 678
QY 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGlu 180
DB 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGTGCTTACACGAAGCCAGGTACACGAAGAAG 738
QY 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
DB 739 CTCAACCTCACACAGCAGCTGCCCTGACTGCAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
QY 189 -----AspGlyAspAsnValLeuLeuThr 196
DB 799 AGCTGCTGGGTCTCGCCCTGGCTCAATGTGTCTACAGATGTGACAATGTCTTCTGACA 858
QY 197 LeuAspValSerGluGlnGlnAspPheSerPheLeuLeuTrpLeuArgProValProAsp 216
DB 859 CTGGATGTCTCTGAGGAGCAGGACTTTTAGCTTCTTACTGTACTCTGCTCCAGTCCCGGAT 918
QY 217 AlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
DB 919 GCTCTCAAAATCTTTGTGGTCAAAAACCTGACTGACCTCAGAACATTTACTTTAAACAC 978
QY 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
DB 979 ACAGACCTGGTTCCTTGCTCTGCAATTCAGGTGTGGTCTGTAGAGCCAGACTCTCAGAGG 1038
QY 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
DB 1039 GTCGAAATCTGCCCTTCCGGGAAGATCCCGGTGCACACAGGAACCTCTGGGCACATAGCC 1098
QY 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
DB 1099 AGGCTGCGGGTACTGTCCCCAGGGGTATGGCAGCTAGATGGCTTGTGTCTGCTGGCGGC 1158
QY 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
DB 1159 AAGGTAAACACTGTGTGGCAGGCACACAGACAGAGTCCCTGCGACGCACTTGTGGCACCA 1218
QY 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
DB 1219 GTGCCCCAGAAACCGCCACTGTGTAATGAGCCACCAAGATTTCCAGTTGTGTGGCAGGCCAC 1278
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
DB 1279 CCCAACCTCTGTGTCCAGGTGAGCACTGGGAGAGGTTCAGTCAAGCGTGTGTGTGG 1338
QY 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
DB 1339 GCTGACTCTTGGGGCCCTTCAAGGATGATATGCTGTGTAGTGGAGATGAAACCCGCGCTC 1398
QY 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
DB 1399 AACCAACACATCATGTGTGCCCTTGGAAACCCAGTGGCTGTACACCACTGCCAGCATGGCC 1458
QY 397 SerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCys 416
DB 1459 TCACAGAGAGCTGCTCGCTGGAGAGGAGTGTGCTCAAGACTTCCGATCACACCATGT 1518
QY 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrp 436
DB 1519 ATGCAGCTGTGGAACGATGACAACATGGGATCGCTATGGGCTGCCCCCATGGACAAGTAC 1578
QY 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
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Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCTAGTCTGGGGCTGAGGTACAGATCTGGTCTTACACGAAGCCACAGTACAGAGAG 540
Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 541 CTCACCTCAACAGCAGCTGCCTGACTGCGAGGGTCTTGAAGTCCGGGACAGCATCCAG 600
Qy 189 -----AspGlyAspAsnValLeuThr 196
Db 601 AGCTGCTGGGTCTGCTCCCTGGCTCAATGTGTCTACAGATGGTGCAATGTCTTCTGACA 660
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 661 CTGGATGCTCTGAGGAGCAGGACTTATAGCTTCTTACTGTACCTCGCTCCAGTCCCGGAT 720
Qy 217 AlaLeuLysSerLeuTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 721 GCTCTCAAAATCTTGTGTGTACAAAACCTGACTGAGCTCAGAACATTACTTTAAACAC 780
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
Db 781 ACAGACTGGTTCCTCGCTCTGCAATTCAGGTGGTGGCTAGAGCCAGACTCTTGAGAGG 840
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
Db 841 GTCGAATCTGCCCTTCCGGAGAGATCCCGGTGCACACAGGAACCTCTGGCAGATAGCC 900
Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
Db 901 AGGTGCGGGTACTGTCCCGAGGGTATGGCAGCTAGATGCGCTTGTCTGTCTGCCGGC 960
Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 961 AAGTAACACTGTCTGGCAGGCCACAGACAGAGTCCCTGCCAGCCACTTGTGCCACCA 1020
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1021 GTGCCCCAGAGAAGCAGCCTGTGAATGAGCCACAGATTTCCAGTTGGTGGCAGGCCAC 1080
Qy 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1081 CCCAACTCTGTGTCCAGGTGAGCAGCCTGGGAGAGGTTTCAGCTGCAAGCGGTCTGTGG 1140
Qy 357 AlaAsnSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1141 GCTGACTCTTGGGGCCCTTCAAGGATGATGCTGTGTAGTGAGATGAAGAACCGGCTC 1200
Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1201 AACACACATCAGTCTGTGCTTGGAAACCAGTGGCTGTACACCACTGCCAGATGGCC 1260
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1261 TCCACGAGAGCTGCTCGCTGGGAGAGAGTGTCTGCAAGACTTCCGATCACACCAAGTGT 1320
Qy 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
Db 1321 ATGCAGCTGTGGAAACGATGACAACTGGATTCGCTATGGGCCCTGCCCATGGACAGATAC 1380
Qy 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
Db 1381 ATCCACAGGCGCTGGGTCTTAGTATGGCTGGCTGCTGCTGCTGCTGGCTGGCTGCTTTC 1440
Qy 457 PhePheLeuLeuLeuLysLysAspArgArgLysAlaAlaAlaArgGlySerArgThrAlaLeu 476
Db 1441 TTCTTCTCTCTTCAAAAAAGGACCGCAGGAAGCGGCCGCTGGCTCCCGCACGGCCTTG 1500
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1501 CTCTTCCACTCCGCGCAGGAGGGGCTACAGCGCTCTGGTGGAGCACTGGGCTCCGCG 1560

Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla 516
Db 1561 TTGAGCCAGATGCACCTGGCGGTGGCGGTGGACCTGTGGAGCGCGCGAGCTGAGCGCG 1620
Qy 517 HisGlyValAlaLeuAlaTrpPheHisHisGlnArgArgArgIleLeuGlnGlyGlyVal 536
Db 1621 CACGGAGCCCTAGCTGGTTCCACCCACGACGACGCGGTATCTTGCAGGAGGGTGGCGTG 1680
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db 1681 GTAAATCTTCTTCTTCCGCCCGCGCGGTGGCGGAGTGTGAGTGGCTGAGCTCCAG 1740
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
Db 1741 ACAGTGGAGCCCGGCGCATGATGACGCCCTCGCCGCTGCTGAGTGGCTGCTACCCGAT 1800
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1801 TTCTTCAAGGCGGGCGGACCCGCCGCTAGTCCGGGTCTTCTTCCAGCGGCTGCTGCAC 1860
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 1861 CCAGACTCTGTGCCCTCCCGTTCGCGTTCGCGTCCCGCTCTTCTCCCTGCGCTGCGACTG 1920
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 1921 CCGGCTTCTTCTGATGACTGACAGGAGGCTGTCTTCCCTCCGCGGCGACCCGCGGAC 1980
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 1981 CCGGTGGAAACGAGTGAACCCAGGCGCTGCGGTTCGCGCTGCGACAGCTGTACTTCTACCTCG 2040
Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2041 GAAGCCCCAGGCTGTCTCGAGGAGATGGGACCTGGGACCTGCACTACACTAGAA 2094

RESULT 11

US-10-152-661-487
; Sequence 487, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011C5
; CURRENT APPLICATION NUMBER: US/10/152,661
; PRIOR FILING DATE: 2002-05-20
; PRIOR FILING DATE: 09/866,050
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/221,232
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/206,650
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/312,283
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 09/188,930
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: 09/069,726
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-487

901	AGGCTCGGGTACTGTCCCAAGGGGTATGGCAGCTAGATGCGCTTGTGTCTGCGGGC	960
297	LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro	316
961	AGGTAACACTGTGTGGCAGGCACAGACCAAGAGTCCCTGCCAGCACTTGTGCCACCA	1020
317	ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis	336
1021	GTCCCCCAGAAGAACCCCACTGTGANTGAGCCACACAGATTTCAGTTGTGGCAGGCCAC	1080
337	ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp	356
1081	CCCAACCTCTGTCTCAGAGTGAGACCTGGGAGAGTTTCAGCTGCAAGGTCCTTGTGG	1140
357	AlaAspSerLeuGlyProPheLysAspAspMetLeuValGluMetLysThrGlyLeu	376
1141	GCTGACTCCTTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAGATGAACCGGCCTC	1200
377	AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla	396
1201	AACACACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACACTGCCAGCTGGCC	1260
397	SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys	416
1261	TCCACGAGAGTGTCTGCCCTGGGAGAGGTGTGTCAGACTTCCGATCACACAGTGT	1320
417	MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTr	436
1321	ATGCAGCTGTGGAAAGATGACACATGGGATCGCTATGGCTGCTATGGCGCTTTTC	1380
437	IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe	456
1381	ATCCACAGGCGCTGGTCTAGTATGGCTGCTCTCTTGGCTGGCGGCTTTTC	1440
457	PhePheLeuLeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu	476
1441	TTCTTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1500
477	LeuLeuHisSerAlaAspGlyValaGlyTyrgluArgLeuValGlyAlaLeuAlaSerAla	496
1501	CTCTCCACTCCGCGACGGAGCGGCTACGAGCGTCTGTGGGAGCAGCTGGCTGCCG	1560
497	LeuSerGlnMetProLeuArgValAlaValaAspLeuTrpSerArgGluLeuSerAla	516
1561	TTGAGCCAGATGCCACTCGCGTGGCCGTGGACCTGTGGAGCCGCCGCGAGCTGAGCGG	1620
517	HisGlyAlaLeuAlaTrpPheHisGlnArgArgGlyLeuGlnGlyGlyVal	536
1621	CACGGAGCCCTAGCTGTGTTCCACCACGAGCGAGCCGCTATCTGACGAGGCTGGCGTG	1680
537	ValIleLeuLeuPheSerProAlaAlaValaGlnCysGlnGlnTrpLeuGlnLeuGln	556
1681	GTAAATCTTCTCTCTCCGCGCGCGCTGGCGAGTGTACAGTGGCTGCAGCTCCAG	1740
557	ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp	576
1741	ACAGTGGAGCCCGCGCGCGATGACCGCTCCGCGCTGGCTCAGCTGGCTGACCTCCGAT	1800
577	PheLeuGlnGlyArgAlaThrGlyArgTyrglyValGlyValTyrglyPheAspGlyLeuLeuHis	596
1801	TTCTCTCAAGGCGCGCGCGAGTGTGCTGCGGGTCTACTTCCAGCGGGCTGGCTGCAC	1860
597	ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu	616
1861	CCAGACTCTGTGCCCTTCCCGCTTCCGCTGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT	1920
617	ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp	636
1921	CCGGCTTTCTTGGATGACCTGACGAGGAGCTGTCTCCACTTCCGCGGGGCGAGCCCGCGAC	1980
637	ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer	656
1981	CGGGTGGAAAGAGTGAACCCAGGGCGCTGCGGCTCCGCTTCCAGCTGTACTTCTTACTCTCG	2040

20	MetProValSerTrpPheLeuSerLeuAlaLeuGlyArgAsnProValValValSer	20
60	ATGCCCTGTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTCTCT	60
40	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
120	CTGGAGAGACTGATGGAGCCTCAGGACACTGGACGCTGCTCTCTAGGCTCTCTCTGCCAC	120
60	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
180	CTCTGGATGGTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180
80	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
240	CTAGTGCCTTACCCGCTGCAGACGGAGCTGGTGTGAGGTGTCCACAGAGACATTTGC	240
100	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
300	GCCCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	300
120	GluAlaGlySerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln	120
360	GAAGCTGGAAGTCTGATTCAGAACTCCAGAGTCTAGGAGCGCTCTCTCCAGGCCCGAG	360
140	ValValLeuSerPheGlnAlaTyrglyProIleAlaArgCysAlaLeuLeuGlnVal	140
420	GTGGTGTCTCTCTTCCAGGCTTACCCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420
160	ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
480	CCGCTGACCTGTGTGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	480
180	AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrglyProArgTyrglyGlnLysGlu	180
540	GCTAGTCTTGGGCTGAGGTACAGATCTGCTTCTACAGAGCCAGGTACCGAAGAG	540
188	LeuAsnLeuThrGlnGlnLeuPro-----	188
600	CTCAACCTCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600
196	AspGlyAspAsnValLeuLeuThr-----	196
660	AGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
216	LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrglyLeuArgProValProAsp	216
720	CTGGATGTCTGTGAGGAGCAGGACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	720
236	AlaLeuLysSerLeuTrpTyrglyAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis	236
780	GCTCTCAAACTCTTGTGTACAAAACCTGACTGGACCTCAGAACATTTACTTTAAACCCAC	780
256	ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg	256
840	ACAGACCTGGTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	840
276	ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla	276
900	GTCGAAATCTGCCCCCTTCCGGAGAGTCCCGTGTGCACACAGGAACCTCTGCGACATAGCC	900
296	ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly	296

Qy 657 GluAlaProGlyCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
 Db 2041 GAAGCCCCAGGCTGCTGGAGGATGGACCTGGGACCCCTGCACCTACACTAGAA 2094

RESULT 12
 US-10-416-442A-74
 ; Sequence 74, Application US/10416442A
 ; Publication No. US20040171109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haudenschild, Dominik
 ; APPLICANT: Rose, Larry
 ; APPLICANT: Moseley, Timothy
 ; APPLICANT: Reddi, A. Hari
 ; TITLE OF INVENTION: The Regents of the University of California
 ; TITLE OF INVENTION: IL-17 Receptor-Like Protein, Uses Thereof, and
 ; TITLE OF INVENTION: Modulation of Catabolic Activity of IL-17 Cytokines on
 ; TITLE OF INVENTION: Bone and Cartilage
 ; FILE REFERENCE: 023070-115511US
 ; CURRENT APPLICATION NUMBER: US/10/416.442A
 ; PRIOR FILING DATE: 2003-05-09
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 74
 ; LENGTH: 2331
 ; TYPE: DNA
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: mouse IL-17RL cDNA with untranslated regions
 US-10-416-442A-74

Alignment Scores:
 Pred. No.: 0 Length: 2331
 Score: 3539.00 Matches: 666
 Percent Similarity: 95.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 7
 Query Match: 98.2% Indels: 24
 DB: 8 Gaps: 1

US-10-719-202-2 (1-674) x US-10-416-442A-74 (1-2331)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
 Db 199 ATGCTGTGTCTCTGGTTCCTGTCTCTGGCACTGGGCGGAAACCCCTGTGGTCTCT 258

Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 259 CTGGAGAGACTGATGGAGCTCAGGACACTGCACGCTGCTCTTAGGCTCTCTCTGCTCCAC 318

Qy 41 LeuTrpAspGlyaspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 319 CTCTGGGATGGTACGCTGCTGCTGCTGGAGGCTTCAGTCTGCCCCAGGCGCTGTG 378

Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 379 CTAGTGTCTACCCCTGCGAGAGAGAGCTGGTGTGAGGGTGTCCACGAAGACAGATTGC 438

Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 Db 439 GCCCTCTGTCTGGTGTGGTCCACTTGGCCGTGCTAGTGGCACTGGGCGAGGCTGAA 498

Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
 Db 499 GAAGCTGGAAGTCTGATCAGAACTCCAGAGTCTAGGAACGCTCTCTCCAGGGCCAG 558

Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
 Db 559 GTGGTGTCTCTCTCCAGGCTTACCCCATGCCCGCTGTGCCCTGTGGAGGTCCAGGTG 618

Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
 Db 619 CCCGCTGACCTGGTGCAGCTGGTCCGTGGGTTCTCGGGTATTTGATGTGTTTCGAG 678

Qy 161 AlaSerLeuGlyValGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
 Db 679 GCTAGTCTTGGGCTGAGGTACAGATCTGTCTTACACGAAGCCCGAGTACCAGAAAGAG 738

Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
 Db 739 CTCAACCTCACACAGCAGCTGCTGTGCTGAGGTCCGGGAGCAGCATCCAG 798

Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
 Db 799 AGCTGTGGGTCTGCCCTCGCTCAATGTGTCTACAGATGTGTGACAAATGTCTTCTGACA 858

Qy 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
 Db 859 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACCTGCTGCTGCTGCTGCTG 918

Qy 217 AlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
 Db 919 GCTCTCAATCTTGTGTGTACAAAACCTGACTGGACCTCAGAACATTACTTTAAACCCAC 978

Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
 Db 979 ACAGACTGTGTTCCCTCTGCTCAATTCAAGTGTGGTGTGCTAGAGCCAGACTCTCTGAGAG 1038

Qy 257 ValGluPheCysProPheArgGluAspProGlyValHisArgAsnLeuTrpHisIleAla 276
 Db 1039 GTCGAATTCGCCCCCTTCGGGGGAAGATCCCGGTGCACACAGGAACCTCTGGCAGATAGCC 1098

Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly 296
 Db 1099 AGGCTGGGGTACTGTCCCCAGGGGTATGGCAGCTAGATGGCTGTGCTGTCTGCCGGGC 1158

Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
 Db 1159 AAGGTAACTGTGTGGCAGGACCAGACAGAGTCCCTGCCAGGCACCTGTGTGCCACCA 1218

Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
 Db 1219 GTGCCCCAGAGAAACGCCACTGTGAATGAGCCCAAGATTTCCAGTTGGTGGGAGGCCAC 1278

Qy 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
 Db 1279 CCCAACCTGTGTCTCAGGTGAGCAGCTGGGAGAGGTTTCAGCTGCAGAGGTCTGTGTTGG 1338

Qy 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
 Db 1339 GCTGACTCTTGGGCCCCCTTCAAGGATGATATGCTGTAGTGGAGATGAAACCGGCTC 1398

Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
 Db 1399 AACAAACACATCATGCTGTGCTTGGAAACCCAGTGGCTGTACACACTGCCCCAGCATGGCC 1458

Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
 Db 1459 TCCACGAGAGTGTCTGCTGGGAGAGGAGTGTCTGCAGACTTCCGATCAGCCAGTGT 1518

Qy 417 MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
 Db 1519 ATGCAGCTGTGGAAACGATGACAACATGGGATCGTATGGCGCTGCCCATGGAGCAAGTAC 1578

Qy 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
 Db 1579 ATCCAGCGCGTGGGTCTCTAGTATGGCTGGCTGCTACTCTCTGGCTGGCGGCTTTTC 1638

Qy 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476

DB:	3	Gaps:	0
US-10-719-202-2 (1-674) x US-09-899-471-3 (1-2022)			
Qy	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20
Db	1	ATGCCNGTWSNTGGTYTNTWNSNTGNGNMGNAAYCCNGTNGTNGTWSN	60
Qy	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
Db	61	YTNMGNGNTNATGCGCCNCARGAYACNGCMNGTGYWSNTGNGNTWNTWSNTGTTCAY	120
Qy	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
Db	121	YTNMGNGAYGNGAYGTNTGTNTGTYTNCNGGWSNTYTCARWSNCCNGCCNGGNTN	180
Qy	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
Db	181	YTNGTNCCNACNMGNNTNCARACNGARYTNGTNTYTNMGNTGYCCNCARAAACNGAYTG	240
Qy	81	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
Db	241	GCNTYTNMGNTNMGNTGTGTNTGTCAYTNGCNGTNCAYGNCAYTGGGCGNARGCNGAR	300
Qy	101	GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln	120
Db	301	GARGCNGNAAARWSNGAYWSNGARYTNCARGARWSNMGNAAAYGCMWSNTNCCARGCNCAR	360
Qy	121	ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuGluValGlnVal	140
Db	361	GTNGTNTYTNSTNTYTCARGCNTAYCCNATGCMNGNTGYGNTYTNNGARGTNCARGTGN	420
Qy	141	ProAlaLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
Db	421	CCNGCNGAYTNGTNCARCCNGCNGCARGWSNCTNGCNGWSNCGTNTTYGAYTGYTYTCAR	480
Qy	161	AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu	180
Db	481	GCNWSNTYTNMGNGCNGARGTNCARATHTGGWSNTAYACNAAARCCNMGNMTAYCARAARGAR	540
Qy	181	LeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSer	200
Db	541	YTNAAYTNTACNCARCARYTTCGCCNGAYGNGAYAYAGTNTYTNACNTYTNNGAYTGNWSN	600
Qy	201	GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer	220
Db	601	GARGCARGAYTNTYTNNTYTNNTAYTNTMGNCNGTNCNGGAYGCNTYTNAAARWSN	660
Qy	221	LeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal	240
Db	661	YTNTGGTAYAAARAYTNTACNGCNCARAAAYATHACNTYTNAAAYACACNGAYTNGTN	720
Qy	241	ProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheCys	260
Db	721	CCNTGYTNTGYATHCARGTNGTGGWSNTNGARCCNGAYWSNGARMGNGTNGARTTYTGY	780
Qy	261	ProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuArgVal	280
Db	781	CCNTTYVMNGARGAYCCNGGNGCNCAYMGNAAAYTNTGGCAYATHGCMNGNTYTNMGNGTN	840
Qy	281	LeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu	300
Db	841	YTNWSNCCNGGNGTNGGCARVTNGAYGNCNTGYTGYTTCNGGNGAARGTACNTYN	900
Qy	301	CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProValProGlnLys	320
Db	901	TGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCTYNTGTNGTNCNGCNCNGCNCARAR	960
Qy	321	AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys	340
Db	961	AAAGCNCNGTNAAYGARGCNCARGAYTTCYARYTNGTNGCNGCNGAYCCNAAAYTNTGY	1020
Qy	341	ValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeu	360

Db	1639	TTCTTCTCTCTTCTTAAAGGACCGCAGGAAGCGGCCCTGCTCCCGACGGCCTTG	1698
Qy	477	LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla	496
Db	1699	CTCTCTCACTCGCGCAGCGAGCGGGCTACGAGCGTCTGGTGGAGCACTGGCGCTCGCG	1758
Qy	497	LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAla	516
Db	1759	TTGAGCCAGATGCCACTCGCGGTGGCGGTGACCTGTGGAGCCCGCGGAGCTGAGCGCG	1818
Qy	517	HisGlyAlaLeuAlaTrpPheHisGlnArgArgIleLeuGlnGluGlyVal	536
Db	1819	CACGGAGCCCTAGCTGTCTCCACCACGACGAGCGCGTATCTTCGACGAGGGTGGCGTG	1878
Qy	537	ValIleLeuLeuPheSerProAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln	556
Db	1879	GTAATCTCTCTCTCGCGCGCGCGTGGCGCAGTGTACGAGTGGCTGCAGCTCCAG	1938
Qy	557	ThrValGluProGlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAsp	576
Db	1939	ACAGTGGAGCCCGCGCGCGCATGACGCCCTCGCGGCTGGCTCAGCTGCTACCCGAT	1998
Qy	577	PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuHis	596
Db	1999	TTCTTGCAAGCGCGCGACCGCGCTACGTCGGGGTCTACTTCGACGGGCTGCTGCAC	2058
Qy	597	ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu	616
Db	2059	CCAGACTCTGTGCCCTCCCSSTTCGCGTGGCGCGCTCTCTCTGCTGCTGCTGCTG	2118
Qy	617	ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp	636
Db	2119	CCGGCTTCTTGATGCACTGCAGGAGGCTGCTCCACTTCGCGGGCGACCCCGCGAC	2178
Qy	637	ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSer	656
Db	2179	CGGGTGGAAACGATGACCCAGCSCCTGCGGTCCCCCTCGGACGCTGTACTTCTAGCTCG	2238
Qy	657	GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu	674
Db	2239	GAASCCCGAGGCTCTCGGAGGATGGGACCTGGGACCTGGGACCTACACTAGAA	2292

RESULT 13
US-09-899-471-3
; Sequence 3, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc_feature
; LOCATION: (1)...(2022)
; OTHER INFORMATION: n = A,T,C or G
US-09-899-471-3

Alignment Scores:
Pred. No.: 6.49e-284 Length: 2022
Score: 2666.00 Matches: 484
Percent Similarity: 71.8% Conservative: 0
Best Local Similarity: 71.8% Mismatches: 190
Query Match: 74.0% Indels: 0

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Db 1021 GTNCARGTWSNACNTGGGAARGTNCARYTNCARGCNTGYWSNTGGCGNGAYWSNYTN 1080
Qy 361 GlyProPheLysAspAspMetLeuValGluMetLysThrGlyLeuAsnAsnThrSer 380
Db 1081 GGNCCNTTYAARGAYGATGTNTYNTGTNGTARATGAARACNGGNYTNAAYAAACWNSN 1140
Qy 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
Db 1141 GTNTGYCNYTNGARCCNWSNGNTGYACCCNTYTNCCNWSNATGGCNWSNACNMGNGCN 1200
Qy 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTyr 420
Db 1201 GCNMGNTTNGCGARGARYTNTYTCARGAYTNTYTNMGNSNCAYCACTGYATGCARYTNTGG 1260
Qy 421 AsnAspPheAsnMetGlySerLeuTyrAlaCysProMetAspLysTyrIleHisArgArg 440
Db 1261 AAYGAYGAYAAATGGGNSNYTNTGGCGTGYCCNATGGAYAAATAYATHCAVMGNGN 1320
Qy 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu 460
Db 1321 TGGGTNTGTNTGGYTNCGNTGYTNTYTNMGNGCGNCTNTTYTNTYTYTNTYTN 1380
Qy 461 LeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSer 480
Db 1381 YTNAAARAARGAYMGNMGNAARGCGNMGNGNMGNSNMGNACGNCYNTYNTYTNCAYSN 1440
Qy 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
Db 1441 GCGAYGGCGGCGNTAYGARMGNTYNTGTGGGNCYTNCGNMGNSGNCYTNWSNCARATG 1500
Qy 501 ProLeuArgValAlaValAspLeuTyrSerArgArgGluLeuSerAlaHisGlyAlaLeu 520
Db 1501 CCNTYTNMGNTGCGTNGAYTNTGGSNMGNGARGYTNWSNCGNCAYGGGNCYTN 1560
Qy 521 AlaTrpPheHisGlnArgArgGlyLeuGlnGluGlyGlyValValIleLeuLeu 540
Db 1561 GCNTGGTTYCAYCAYCARMGNMGMNATHYTNCCARGCGGNGTNGTNTYTN 1620
Qy 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
Db 1621 TTYWSNCCNGCGTNGCNCARTGYCARCTGGYTNCCARYTNCARACNGTNGARCCN 1680
Qy 561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
Db 1681 GGNCCNAYGAYCNYTNGCGNCGTGTWSNTGYGTNTYTNCCNGAYTYYTNTCARGGN 1740
Qy 581 ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal 600
Db 1741 MNGCNACNGNMGNTAYGTNGGNTNTAYTYTGAYGNTYTNCAACCNGAYWSNGTN 1800
Qy 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
Db 1801 CCNMSNCCNTYTMGNTGNGCNCNTYNTYTNYSNTYTNCCNACNARYTNCNCGCNTTYTN 1860
Qy 621 AspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
Db 1861 GAYGNTTNCARGNGGNTGYWSNACNWSNCGNMGNGNCGNCGNAYMGNGTNGARMGN 1920
Qy 641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
Db 1921 GTNACNARGCNYTNMGNSNCGNYTNGAYWSNTGYACNWSNWSNWSNARGCGNCCNGN 1980
Qy 661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 1981 TGYTGYGARGARTGGGAYTNGGNCNTGYACNACNTNGAR 2022
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RESULT 14

US-10-719-202-3

; Sequence 3, Application US/10719202

; Publication No. US20040121389A1

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

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; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; - PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2022)
; OTHER INFORMATION: n = A,T,C or G
US-10-719-202-3
```

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Alignment Scores:
Pred. No.: 6,49e-284 Length: 2022
Score: 2666.00 Matches: 484
Percent Similarity: 71.8% Conservative: 0
Best Local Similarity: 71.8% Mismatches: 190
Query Match: 74.0% Indels: 0
DB: 8 Gaps: 0
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US-10-719-202-2 (1-674) x US-10-719-202-3 (1-2022)

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Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 1 ATGCCGTTWSNTGGTYYTNTYTNWSNTGNCYTNMGNGMNAAYCCGNTGNTGNTWSN 60
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 61 YTNGARMGNTYNTATGGARCCNCCARGAYACNCGMNGTGYWSNTGNGNTYTNWSNTGYCAY 120
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTN TGAGYGGNGAYGTNTYNTGTYTNCNCGNWSNYTNCARWSNCGNCCNGGNCNGTN 180
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 YTNGTNCCNACNMGNTNCARACNGARYTNTGTYTNCNCGNWSNYTNCARACNACNGATGY 240
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 241 GCNYTNMGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 300
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GARGCNGNAAARWSNGAYTWSNGARYTNCARGARWSNMGNAAAYGCNWSNYTNCARGCNCAR 360
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 361 GTNGTNTYTNWSNTTYCARGCNTAYCCNATHGCMNGMTGYCMTNTYTNGTNGARGTNCARGTN 420
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 421 CCNCGNCAAYTNTGNTNCARCCNCGNCCARGWSNGTNGNWSNCGNCTNTTYGATGYTGYT 480
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCNWSNYTNGGNGCNGARGTNCARATHTGGWSNTAYACNAAARCCNMGNTAYCARAARGAR 540
Qy 181 LeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSer 200
Db 541 YTNAAAYTTNACNCCARCYTNCNCGAYGGNGAYAAAGTNTYTNACNNTYTNNGAYGTNWSN 600
Qy 201 GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer 220
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601 GARGARCARGAYTTYSNTTYYTNTAYTNTMGNCNGTCCNGAYGCNNTAARWSN 660
221 LeuTTPYrlysaAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal 240
661 YTWGGTAYARAAYTNTACNGCNCARAAVATHACNNTAAYCAYACNGAYTNTGNTN 720
241 ProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheCys 260
721 CCNTGYTNTGYATHCARGTGTGWSNTYNGARCCNGAYGWSNGARMGNGTNGARTTYTG 780
261 ProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuA-gVal 280
781 CCNTTYMGNGARGAYCNGCNGCNCAYMGNAAYTNTGGCAYATHGCMNGNMTMGNTN 840
281 LeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyIysValTrpLeu 300
841 YTNWSCNGCNGTNTGTCARYTNGAYGCNCNTGYTTCNGCNGNAARGTACNNTYN 900
301 CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGlnIlys 320
901 TGYTGGCARGCNCNGAYCARWSCNCTGYCARCNYTNGTNGCNCNGTCCNGTCCNARAR 960
321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 340
961 AAYGCNACNGTNAAYGARGCNCARGAYTTCARYTNGTNGCNGCNCAYCCNAAYTNTGY 1020
341 ValGlnValSerThrTrpGluIysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeu 360
1021 GTNCARGTNSNACNTGGARAARGTNCARYTNCARGCNGTGYWSNTGGCNGAYWSNTN 1080
361 GlyProPheIysAspAspMetLeuLeuValGluMetIysThrGlyLeuAsnThrSer 380
1081 GNCNCTTYAARGAYGAYATGYTNTGTNGTNGARATGAARACNGGNYTNAAYAAACNWSN 1140
381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
1141 GTNTGYCNYTNGARCCNWSNGNTGYACNCCNYTNCNWSNATGCGCWSNACNMGNCN 1200
401 AlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 420
1201 GCMNGNTYGGNGARGARYTNTNCARGAYTNTMGWSNCAYCARTGYATGCARYTNTGG 1260
421 AsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspIysThrIleHisArgArg 440
1261 AAYGAYAAVATGGGNSNTYNTGGCNGTGYCCNATGGAYAAATAYATHCAYMGNGN 1320
441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePheLeuLeu 460
1321 TGGGTNTGTNTGGYTGNGTGYTNTYNTYNGCNGCNGCNYTNTYTYTYTYTYTYTNTN 1380
461 LeuIysIysAspArgArgIysAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
1381 YTNARAARGAYMGNGMNGCNGCNGCNGMNGMNGNACNCTNTNTNTNTNCAYSN 1440
481 AlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
1441 GCNGAYGGCNGGNTAYARGMNGYNTGTNGCNGCNGTNGCNGCNGCNYTNTYTYTYTYTYTNTN 1500
501 ProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeu 520
1501 CCNTYMGNTGCGTNGTNGAYTNTGWSNMGNGMNGARYTNTNSNGCNCAYGGNGCNYT 1560
521 AlaTrpPheHisGlnArgArgArgIleLeuGlnGluGlyValValIleLeuLeu 540
1561 GCNTGGTTCAYCAYCARMGNGMNGNATHYTNCARGGNGGNGTNGTNGTNTYTYTNTN 1620
541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
1621 TTYWSNCCNGCNGCNGTNGCNCARTGYCARCARTGGYTNCARYTNCARACNGTNGARCCN 1680
561 GlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
1681 GNCNCNCAYGAGCNYTNGCNGCNGTNGTNTNSNTGYGTNTYNTCCNGAYTYTYTYTNCARGN 1740

581 ArgAlaThrGlyArgTyrrValGlyValTyrrPheAspGlyLeuLeuHisProAspSerVal 600
1741 MNGCNCNCGNMGNTAYGTNGGNTNTAYTYTGAYGNGNTYNTNCAICCGAYWSNGTN 1800
601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
1801 CCNWSNCCNTTYMGNTGTCNCNTYNTYWSNTYNTCCNACNCACTYTCNCNGCNTTYTN 1860
621 AspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
1861 GAYGCNNTCARGGNGTGYWSNACNWSNGCNGCNGCNGCNGAYMGNTGNGARWN 1920
641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
1921 GTNACNARGCNYTNGNWSNCGTNGAYWSNTGYACNWSNWSNWSNGARGCNCNGCN 1980
661 CysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
1981 TGYTGYGARGATGGAYTYTNGCNCCTGYACNACNTNGAR 2022
RESULT 15
US-09-899-471-6
; Sequence 6, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:5.
; NAME/KEY: misc feature
; LOCATION: (1)...(2094)
; OTHER INFORMATION: n = A,T,C or G
US-09-899-471-6
Alignment Scores:
Pred. No.: 1,86e-281 Length: 2094
Score: 2644.00 Matches: 484
Percent Similarity: 69.3% Conservative: 0
Best Local Similarity: 69.3% Mismatches: 190
Query Match: 73.3% Indels: 24
DB: 3 Gaps: 1
US-10-719-202-2 (1-674) x US-09-899-471-6 (1-2094)
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QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 61 YTNARGMNGYTNATGARGCNCARGAYACNGCNGMTGYWSNTYNGTNGTNSNTGYCAY 120
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTNWGGGAYGGNGAYGTNTTGYTTCNCGGNSNTYNTCARWSNCGCNCNGCNGCNGTN 180
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIysThrAspCys 80
Db 181 YTNGTTCNACNMGNTNCARACNGARYTNGTNTYNTMGNTGYCCNARACNGAYTGY 240
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisIleTrpAlaGluProGlu 100

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GenCore version 5.1.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 08:33:35 ; Search time 951 Seconds
(without alignments)
7412.138 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MPVSWFLSLALGRNPVVVS.....SSEAPGCCSEWDLGPCTTLE 674

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs05p
-USER=US10719202 @CGN 1.1 1147 @runat_16082006_095630_13218 -NCPU=6 -ICPU=3
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3605	100.0	2256	6 AAD24220	Aad24220 Murine cy
2	3583	99.4	2328	6 AAD24222	Aad24222 Murine cy
3	3572.5	99.1	2269	15 AEF05372	Aef05372 Mouse zcy

ALIGNMENTS

RESULT 1
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ID AAD24220 standard; DNA; 2256 BP.

XX
AC AAD24220;
XX AAD24220;
DT 17-MAY-2002 (first entry)
XX Murine cytokine receptor Zcytor14 DNA.
DE Murine cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW gene therapy; protein therapy; gene; ds.
XX Mus sp.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
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FT sig_peptide
197..2256
/tag= b
FT mat_peptide
257..2218
/tag= c
FT
FT /product= "Mature cytokine receptor, Zcytor14"
XX
XX WO200204519-A2.
XX

Aef05376 Mouse zcy
Aas18132 Mouse DNA
Aeb55651 Mouse DCS
Ab134982 Murine cd
Abk86568 Murine int
Aad24221 Murine cy
Aad24223 Murine Zc
Aas18133 Mouse DCR
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Aad47894 Human cyt
Aef05348 Human IL1
Aas46223 Human DNA
Aaf92138 Human PRO
Aas09515 Human CDN
Ab874458 Human CDN
Ab189253 Human PRO
Ab195742 Human ang
Aca89673 cDNA enco
Aca73683 Human sec
Aca05998 Human sec
Aca66832 cDNA enco
Aca91244 Novel hum
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Acd25349 Human sec
Acf00398 Human sec
Aca60443 Novel hum
Aad72455 Novel hum
Acd04979 Novel hum
Acd18440 Human sec
Acd08447 Human sec
Aca88881 Novel hum
Aca70323 Human sec
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Acc74460 Human sec
Acd16088 Human sec
Acd25656 Novel hum
Acd18133 Human sec
Acc88420 Human sec

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PF	05-JUL-2001; 2001WO-US021344.	557	GTGGTGCTCTCTTCCAGGCTACCCCATCGCCGCTGTGCCCTGGAGGTCCAGGGT	616
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PR	06-JUL-2000; 2000US-021646P.	141	ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
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XX	(ZYMO) ZYMOGENETICS INC.	617	CCCGCTGACCTGGTGCAGCTGGTCCGTGGGTCTCGCGTATTTCGACTGTTTCGAG	676
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XX	Gao Z;	161	AlaSerLeuGlyAlaGluValGlnIleTyrSerTyrThrLysProArgTyrGlnLysGlu	180
PI				
XX	WPI; 2002-179701/23.	677	GCTAGTCTTGGGGCTGAGGTACAGATCTGGTCTTACACGAAGCCAGGTACCAAAAGAG	736
DR	P-PSDB; AAE14559.			
DR		181	LeuLeuLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSer	200
XX				
XX	New murine cytokine receptor, Zcytor14, and polynucleotides encoding the	737	CTCAACCTCACACAGCAGCTGCCTGATGGTGACATGCTCTTCGACACTGGATGTCCT	796
PT	receptor, useful for treating inflammation, specifically rheumatoid			
PT	arthritis, and as educational tools or in research.	201	GluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer	220
XX				
PS	Claim 8; Page 87-90; 99pp; English.	797	GAGGAGCAGGACTTTAGCTTCTTACTGTACTCTCCAGTCCCGGATGCTCTCAAAATCC	856
XX				
CC	The present sequence is murine cytokine receptor Zcytor14 DNA. The	221	LeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal	240
CC	Zcytor14 polypeptide is useful for identifying or isolating Zcytor14			
CC	ligands, in preparing antibodies, in identifying proteins or peptide	857	TTGTGGTCAAAACCTGACTGGACCTCAGAACATTACTTTTAAACACACAGACCTGGT	916
CC	cleavage sites, in amino acid sequence analysis, and in monitoring			
CC	biological activities of both the native and tagged protein in vitro or	241	ProCysLeuCysIleGlnValTyrSerLeuGluProAspSerGluArgValGluPheCys	260
CC	in vivo. Polypeptides having Zcytor14 activity can be used to treat			
CC	inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may	917	CCCTGCCTCTGCATTTCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	976
CC	be used as educational tool in genetics, molecular biology, protein			
CC	chemistry and antibody production analysis, in the preparation of	261	ProPheArgGluAspProGlyAlaHisArgAsnLeuTyrHisIleAlaArgLeuArgVal	280
CC	expression constructs for bacterial, viral or mammalian expression, in			
CC	determining mRNA and DNA localisation of Zcytor14 polynucleotide in	977	CCCTTCCGGGAAGATCCCGGTGCACACAGGAACCTCTGGCACATAGCCAGGCTCGGGTA	1036
CC	tissues, for identifying related polynucleotides and polypeptides by			
CC	nucleic acid hybridisation, in linkage-based testing for various diseases	281	LeuSerProGlyValTyrGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu	300
CC	in murine models, and to determine whether a subject's chromosomes			
CC	contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes	1037	CTGTCCCGAGGGGTATGGCAGCTAGATGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1096
CC	are useful for in vivo diagnosis, and for detecting and localising			
CC	Zcytor14 gene expression in tissue samples	301	CysTyrGlnAlaProAspGlnSerProCysGlnProLeuValProValProGlnLys	320
XX				
SQ	Sequence 2256 BP; 416 A; 706 C; 679 G; 455 T; 0 U; 0 Other;	1097	TGCTGGGAGGCCACAGACAGAGTCCCTGCCAGCCACTTGTGCCACCATGTCGCCAGAG	1156
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Score:	3605.00	Matches:	674	
Percent Similarity:	100.0%	Conservative:	0	
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DB	197 ATGCCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	256		
QY	21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40		
DB	257 CTGGAGAGACTGATGGAGCCTCAGACACTGACGCTGCTCTCTAGGCCCTCTCTGGCCAC	316		
QY	41 LeuTyrAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60		
DB	317 CTCTGGATGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	376		
QY	61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80		
DB	377 CTAGTGCCTTACCGCCTGCAGACGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	436		
QY	81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTyrAlaGluProGlu	100		
DB	437 GCCCTCGGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	496		
QY	101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgArgAsnAlaSerLeuGlnAlaGln	120		
DB	497 GAAGCTGGAAAGCTCTGATTTCAGAACTCCAGGAGTCTAGGAAAGCCCTCTCTCAGG	556		

677	Db	GCTAGTCTTTGGGGCTGAGGTACAGATTCTGGTCTTACAGAAAGCCAGGTACCGAAGAG	736
181	Qy	LeuAsnLeuThrGlnGlnLeuPro-----	188
737	Db	CTCAACCTCACAGACGCTGCTGACTGCAGGGGTCTTGAAGTCGGGACAGCATCCAG	796
189	Qy	-----AspGlyAspAsnValLeuLeuThr	196
797	Db	AGCTGTGGGTCTGTGCCCTGGCTCAATGTGTCTACAGATGGTGAACAATGTCTTCTGACA	856
197	Qy	LeuaspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp	216
857	Db	CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACTCTCGSTCCAGTCCCGGAT	916
217	Qy	AlaLeuIysSerLeuTrpTyrIysAsnLeuThrGlyProGlnAsnIleThrIleuAsnHis	236
917	Db	GCTCTCAAAATCCTTGTGGTACAAAAACCTGACTGGACCTCAGAAATTAACCTTTAAACCCAC	976
237	Qy	ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg	256
977	Db	ACAGACCTGGTCTCCCTGCTCTGCATTCAGGTGTGTGTCTGCTTAAGCCAGACTCTTGAGAGG	1036
257	Qy	ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla	276
1037	Db	GTCGAATTCGCCCTCTCCGGGAAGATCCCGGTGCACACAGAAACCTCTGGCACAATAGCC	1096
277	Qy	ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly	296
1097	Db	AGGCTGGGGGTACTGTCTCCAGGGGTATGCGACTAGATGCGCTTGTCTGTCTGCGGGC	1156
297	Qy	LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro	316
1157	Db	AAAGTTAACATGTGCTGGCAGGCCACAGACAGAGTCCCTGCCAGCACTTGTGTCACCA	1216
317	Qy	ValProGlnIysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValalagIyHis	336
1217	Db	GTGCCCCAAGAAAGCGCACCTGTGAATGAGCCCAAGAGATTTCAGTGTGTGGGAGGCCAC	1276
337	Qy	ProAsnLeuCysValGlnValSerThrTrpGluIysValGlnLeuGlnAlaCysSerTrp	356
1277	Db	CCCAACCTCTGTGTGTCCAGGTGAGCACCTGGGAGNAGGTTCCAGTGCAGCGTGTCTGTGG	1336
357	Qy	AlaAspSerLeuGlyProPheIysAspAspMetLeuLeuValGluMetIysThrGlyLeu	376
1337	Db	GCTGACTCTTTGGGGCCCTTCAAGGATGATATGCTGTAGTGAGATGAAACCGGCCTTC	1396
377	Qy	AnaAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla	396
1397	Db	AACAACACATCATGCTGTGTCCCTTTGGNACCAGTGGCTGTACACCACTGCCACAGATGGCC	1456
397	Qy	SerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCys	416
1457	Db	TCCACGAGAGCTGCTCGCTGGCAGAGAGGTGTGTCGAAGACTTTCGATCACAACCAAGTGT	1516
417	Qy	MetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspIysTyr	436
1517	Db	ATGCGAGCTGTGGAACGATGACAACATGGGATCGCTATGGGCTGTCCCACTGGACAGATAC	1576
437	Qy	IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe	456
1577	Db	ATCCACAGGCGCTGGGTCTTAGTATGGCTGGCCTGCTACTCTTTGGCTGGGGGCTTTTTC	1636
457	Qy	PhePheLeuLeuLeuIysIysAspArgIysAlaAlaArgGlySerArgThrAlaLeu	476
1637	Db	TTCTTCTCTCTTCTATAAAAGACCGCAGGAAGCGGCCCGTGGCTTCCGCACGGCCCTTG	1696
477	Qy	LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla	496
1697	Db	CTCTTCCACTCCGCGCAGCGGGCTACGAGCGTCTGTGTGGAGAGCACTGGCTCCGCG	1756
497	Qy	LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla	516
1757	Db	TTGAGCGCAGATGCCATGCGCGTGGCGGTGGACACTGTGTGAGCCGCCCGCAGCTGAGGCGG	1816

Qy	517	HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgileLeuGlnGluGlyGlyVal	536		
Db	1817	CAGGAGCCCTAGCCTTGGTTCCACACACGACGACGCCGATCTCTGCAGGAGGTTGGCGTG	1876		
Qy	537	ValileLeuLeuPheSerProAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln	556		
Db	1877	GTAATCTCTTCTTCGCGCGCGCGTGGCGCAGTGTACGACAGTGGCTGCAGCTCCAG	1936		
Qy	557	ThrValGluProGlyProHisaspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp	576		
Db	1937	ACAGTGAGAGCCCGGCGCGCATGACGCCCTCGCCCGCTGGCTCAGCTCGTGTACCCGAT	1996		
Qy	577	PheLeuGlnGlyArgAlaThrGlyArgYrValGlyValYrPheaspGlyLeuLeuHis	596		
Db	1997	TTCTCTGCAAGCGCGGCGACCGGCGCTACGTGGGGTCTTACTTCGACGCGCTGCTGCAC	2056		
Qy	597	ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu	616		
Db	2057	CCAGACTCTGTGCCCTCCCGCTTCGCGCTCGCCCGCTCTTCTCCCTGCCACGACGCTG	2116		
Qy	617	ProAlaPheLeuaspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp	636		
Db	2117	CCGGCTTTCTTGGATGACATCGACGGAGGCTGTCCACTTCGCGGGCGACCGCGGAC	2176		
Qy	637	ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuaspSerCysThrSerSerSer	656		
Db	2177	CGGGTGGAAACGAGTGACCCAGGCGCTCGGTCGCGCTGGACAGCTGTACTTCTAGCTCG	2236		
Qy	657	GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu	674		
Db	2237	GAAGCCCGAGGCTGCTCGAGGAATGGACCTGGGACCTTGCACTACACTAGAA	2290		
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AEF05372					
ID	AEF05372 standard; cDNA; 2269 BP.				
XX	AEF05372;				
DT	23-FEB-2006 (first entry)				
XX	Mouse zcytoR14 variant cDNA SEQ ID NO 25.				
XX	antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;				
KW	antiarthritic; dermatological; aniciporiatic; antibacterial;				
KW	immunosuppressive; antimicrobial; substrate inhibition; therapeutic;				
KW	inflammatory bowel disease; asthma; respiratory disease;				
KW	ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;				
KW	gastrointestinal disease; arthritis; antiarthritic;				
KW	musculoskeletal disease; psoriasis; antipsoriatic;				
KW	dermatological disease; immune disorder; atopic dermatitis;				
KW	dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;				
KW	antibacterial; immunosuppressive; infection; zcytoR14; mutant;				
KW	coding sequence; ss.				
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FT	FT	/product= "Mouse zcytoR14 variant "			
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FN	W02005123778-A2.				
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PD	29-DEC-2005.				
XX	XX				
PR	10-JUN-2005; 2005WO-US020521.				
XX	XX				
PR	10-JUN-2004; 2004US-0578805P.				
XX	XX				
PA	(ZYMO) ZYMOGENETICS INC.				
XX	XX				
PI	Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z.				

PI Jaspers SR, Billsborough J;
 DR WPI; 2006-067457/07.
 DR P-PSDB; ABP05373.
 XX
 PT New isolated soluble receptor comprises at least one Zcytor14 subunit,
 PT useful for treating an inflammatory disease, e.g. asthma, inflammatory
 PT bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
 PT psoriasis.
 XX
 PS Example 28; SEQ ID NO 25; 205pp; English.
 XX
 CC The invention describes an isolated soluble receptor comprises at least
 CC one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
 CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
 CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
 CC ID NO. 24) given in the specification. Also described are: an isolated
 CC soluble receptor comprising Zcytor14, where Zcytor14 comprises a
 CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
 CC the pro-inflammatory activity of either IL-17A comprising fully defined
 CC 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
 CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
 CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
 CC and where the antibody or antibody fragment reduces the pro-inflammatory
 CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
 CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
 CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
 CC role; and treating a pathological condition in a subject associated with
 CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
 CC subunit is useful for treating an inflammatory disease, e.g. asthma;
 CC chronic inflammatory disease selected from inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
 CC psoriasis; or acute inflammatory disease selected from endotoxemia,
 CC septicemia, toxic shock syndrome, or infectious disease. This sequence
 CC represents a mouse IL-17A and IL-17F receptor zcytor14 variant.
 XX
 SQ Sequence 2269 BP; 405 A; 713 C; 685 G; 466 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,56e-251 Length: 2269
 Score: 3572.50 Matches: 671
 Percent Similarity: 98.4% Conservative: 1
 Best Local Similarity: 98.2% Mismatches: 2
 Query Match: 99.1% Indels: 9
 DB: 15 Gaps: 1
 US-10-719-202-2 (1-674) x ABP05372 (1-2269)
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 Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 257 CTGGAGAGACTGATGGAGCCTCAGGACACTGCAGCTGCTCTCTAGGCCTCTCTGCCAC 316
 Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 317 CTCGGGATGTGACGTGCTCGCTGCTGGAGCCCTCCAGTCTGCCAGGCCCTGTG 376
 Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 377 CTAGTGCTACCCGCTGCAGACGGAGCTGGTGTGAGGTGTCCACAGACAGATTGC 436
 Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 Db 437 GCCCTCTGTGTCGTGTGCTGCCTTGGCCGTGCATGGGCACCTGGCGCAGAGCCTGAA 496
 Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAenAlaSerLeuGlnAlaGln 120
 Db 497 GAAGCTGGAAAGTCTGATTTCAGAACTCCAGAGGTCTAGGAACGCCTCTCTCCAGGCCAG 556
 Qy 121 ValValLeuSerPheGlnAlaTyProIleAlaArgCysAlaLeuLeuGluValGlnVal 140

Db 557 GTGGTGTCTCTCTTCCAGGCTATCCCATCGCCGCTGTGCCCTGTGGAGGTCCAGGTG 616
 Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
 Db 617 CCCTGTACCTGGTGTGAGCCTGTGTAGTCCGTGGGTCTCGGGTATTTGACTGTTTCGAG 676
 Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTrpGlnLysGlu 180
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 Qy 181 LeuAsnLeuThrGlnGlnLeuPro-----AspGlyAsp 191
 Db 737 CTCAACCTCACACAGCAGCTGSCCTGTCTGCCCTGGCTCAATGTGCTTACAGATGGTGAC 796
 Qy 192 AsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPheLeuLeuTrpLeu 211
 Db 797 AATGTCTTCTGACACTGGATGTCTGAGAGCAGGACTTTAGCTTCTTACTGTACTCTG 856
 Qy 212 ArgProValProAspAlaLeuLysSerLeuTrpTrpLysAsnLeuThrGlyProGlnAsn 231
 Db 857 CGTCCAGTCCCGGATGCTCTCAATCTTGTGTGTACAAAAACCTGACTGGACCTCAGAAC 916
 Qy 232 IleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGlu 251
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 Qy 252 ProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 271
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 Qy 272 LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaPro 291
 Db 1037 CTCTGGCACATAGCCAGCTGCGGGTACTGTCTCCCGAGGGGTATGGCAGCTAGATGCGCCT 1096
 Qy 292 CysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGln 311
 Db 1097 TGTCTGTCTGCGGGCAAGGTAAACACTGTGTGTGGCAGCACACAGACAGAGTCCCTGCCAG 1156
 Qy 312 ProLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGln 331
 Db 1157 CCACCTTGTGTCACAGTGGCCCCAGAGACGCCACTGTGAATGAGCCACAGATTTTCAG 1216
 Qy 332 LeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeu 351
 Db 1217 TTGGTGGCAGGCCACCCCACTCTGTGTCCAGGTGAGCACCTGGGAGAGGTTTCAGCTG 1276
 Qy 352 GlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGlu 371
 Db 1277 CAAGCGTGTGTGGGCTGACTCTCTTGGGGCCCTTCAAGGATGATATGCTGTAGTGGAG 1336
 Qy 372 MetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrPro 391
 Db 1337 ATGAAACCCGCTCAACACATCAGTCTGTGCTTGGAAACCCAGTGGCTGTACACCA 1396
 Qy 392 LeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspPhe 411
 Db 1397 CTGCCACGATGGCTCCACGAGGCTGCTCGCTGGGAGAGGAGTGTGCTGCAAGACTTC 1456
 Qy 412 ArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCys 431
 Db 1457 CGATCACACAGGTATGACGCTGTGGACGATGGAACGATGCAACATGGATCGCTATGGCCCTGC 1516
 Qy 432 ProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeu 451
 Db 1517 CCATGGACAAAGTACATCCACAGCGCTGGGTCTTAGTATGGGTGGCTGCTGCTACTCTTG 1576
 Qy 452 AlaAlaAlaLeuPhePhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGly 471
 Db 1577 GCTGGCGCGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1636
 Qy 472 SerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLeuValGly 491

Db 1637 TCCGCGACGGCTTGCTCTCCACTCCGCGCAGCGGGCTACGAGCGTCTGTTGGGA 1696
Qy 492 AlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArg 511
Db 1697 GCATCTGGGTCGGCTTGAGCCAGATGCACTGCGCGTGGCGTGACCTGTGGAGCGC 1756
Qy 512 ArgGluLeuSerAlaHisGlyValAlaLeuAlaTrpPheHisGlnArgArgArgIleLeu 531
Db 1757 CGCAGAGCTGAGCGGCGACGAGCGCTAGCTGCTTCTCTGCGCGCGCGTGGCGCAGTGTACG 1816
Qy 532 GlnGluGlyGlyValValIleLeuLeuPheSerProAlaValAlaGlnCysGlnGln 551
Db 1817 CAGGAGGCTGGCGTGGTAACTCTTCTCTGCGCGCGCGTGGCGCAGTGTACG 1876
Qy 552 TrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSer 571
Db 1877 TGGCTGCAGCTCCAGACAGTGGAGCGCGCGCGCATGACGCCCTGCGCGCTGAGT 1936
Qy 572 CysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPhe 591
Db 1937 TCGGTGCTACCCGATTTCTGCGAGCGCGGCGCGCGCTACGTCGGGTCTACTTC 1996
Qy 592 AspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSer 611
Db 1997 GACGGGCTGCTGCACCCAGACTCTGTGCCCTCCCGTTCCGCGTCCCGCTCTTCTCC 2056
Qy 612 LeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAla 631
Db 2057 CTGCCCTCGAGCTGCGCGCTTCTCTGAGTACACTGCAGGAGGCTGTCCACTTCGCG 2116
Qy 632 GlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSer 651
Db 2117 GGGCGACCGCGGACCGGGTGAACAGTGAACCGAGCGCTCGCGTCCCGCTGGACAGC 2176
Qy 652 CysThrSerSerSerGluAlaProGlyCysGlyGluTrpAspLeuGlyProCysThr 671
Db 2177 TGTACTTCTAGCTCGGAAGCCCGAGCTGCTGCGAGGAATGGACCTGGGACCTTGCACT 2236
Qy 672 ThrLeuGlu 674
Db 2237 ACATTAGAA 2245
RESULT 4
ID AEF05376 standard; cDNA; 2287 BP.
XX AEF05376;
AC AEF05376;
XX 23-FEB-2006 (first entry)
XX Mouse zcytor14 variant cDNA SEQ ID NO 29.
XX antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
XX antiarthritic; dermatological; antipsoriatic; antibacterial;
XX immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
XX inflammatory bowel disease; asthma; respiratory disease;
XX ulcerative colitis; antiulcer; Crohns disease; gastrointestinal-gen.;
XX gastrointestinal disease; arthritis; antiarthritic;
XX musculoskeletal disease; psoriasis; antipsoriatic;
XX dermatological; endotoxemia; immune disorder; atopic dermatitis;
XX dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;
XX antibacterial; immunosuppressive; infection; zcytor14; mutant;
XX coding sequence; ss.
XX Mus musculus.
XX Key Location/Qualifiers
XX 197..2266
XX /tag= a
XX /product= "Mouse zcytor14 variant"
XX WO2005123778-A2.
XX

PD 29-DEC-2005.
XX 10-JUN-2005; 2005WO-US020521.
XX 10-JUN-2004; 2004US-0578805P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
XX Jaspers SR, Billsborough J;
XX WPI; 2006-067457/07.
XX P-PSDB; AEF05377.
XX New isolated soluble receptor comprises at least one Zcytor14 subunit,
XX useful for treating an inflammatory disease, e.g. asthma, inflammatory
XX bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
XX psoriasis.
XX Disclosure; SEQ ID NO 29; 205pp; English.
XX The invention describes an isolated soluble receptor comprises at least
XX one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
XX comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
XX amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
XX ID NO. 24) given in the specification. Also described are: an isolated
XX soluble receptor comprising Zcytor14, where Zcytor14 comprises a
XX polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
XX the pro-inflammatory activity of either IL-17A comprising fully defined
XX 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
XX amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
XX to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
XX and where the antibody or antibody fragment reduces the pro-inflammatory
XX activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
XX reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
XX afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
XX role; and treating a pathological condition in a subject associated with
XX Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
XX subunit is useful for treating an inflammatory disease, e.g. asthma;
XX chronic inflammatory disease selected from inflammatory bowel disease,
XX ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
XX psoriasis; or acute inflammatory disease selected from endotoxemia,
XX septicemia, toxic shock syndrome, or infectious disease. This sequence
XX represents a mouse IL-17A and IL-17F receptor zcytor14 variant.
XX Sequence 2287 BP; 410 A; 715 C; 696 G; 466 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 5,96e-251 Length: 2287
Score: 3569.50 Matches: 671
Percent Similarity: 97.5% Conservative: 1
Best Local Similarity: 97.4% Mismatches: 2
Query Match: 99.0% Indels: 15
DB: Gaps: 1
US-10-719-202-2 (1-674) x AEF05376 (1-2287)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 197 ATGCTGTGCTCTGTTCTCTGCTGCTTGGCAGTGGCGCGAACCCTGTGCTCT 256
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 257 CTGGAGAGACTGATGAGGCTCAGGACACTGACGCTGCTCTCTAGGCTCTCTCCAC 316
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 317 CTCTGGAGTGTGACGCTGCTCTGCTGCTGGAAGCTTCAGTCTGCCCGAGCCCTGTG 376
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 377 CTAGTGCCTACCCGCTGCGAGGAGCTGCTGAGGTGTCTCAGGTGTCTCAGAGACAGATTGC 436

PD	29-NOV-2001.	141	ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu	160
XX				
PF		619	CCCGTGACCTGGTGCAGCCTGGTCAAGTCTGGTGGTCTGGGGTATTGACTGTTTCGAG	678
XX				
PR	23-MAY-2001; 2001WO-US016767.	161	AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu	180
XX				
XX	24-MAY-2000; 2000US-0206862P.	679	GCTAGTCTTGGGGCTGAGGTACAGATCTGCTCTACACGAAGCCAGGTACACGAAGAG	738
PA	(SCHE) SCHERING CORP.			
XX				
XX		181	LeuAsnLeuThrGlnGlnLeuPro-----	188
PI	Gorman DM;			
XX				
DR	WPI; 2002-106198/14.	739	CTCAACCTCACACAGCAGCTGCCTGACTGCAGGGGTCTTGAAGTCCGGGACAGATCCAG	798
DR	P-PSDB; AAU11354.			
XX		189	-----AspGlyAspAsnValLeuLeuThr	196
PT	Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide	799	AGCTGCTGGGTCTGCCTGGCTCAATGTGTCTACAGATGGTGACAATGCTCTTCGACA	858
PT	useful for detecting antibodies generated in response to presence of			
PT	increased protein levels or immunological disorders.	197	LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp	216
XX				
FS	Disclosure; Page 17-20; 148pp; English.	859	CTGGATGCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACTGCTGCTCCAGTCCCGAT	918
XX				
CC	The invention relates to primate and rodent DNAX cytokine receptor	217	AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis	236
CC	subunit (DCRS) polypeptides and the polynucleotides encoding them. The			
CC	receptors, or their portions may be useful as phosphate labelling enzymes	919	GCTCTCAATCTTGTGGTACAAAACCTGACTGGACCTCAGAACATTAATCTTTAAACAC	978
CC	to label general or specific substrates. The subunits may also be			
CC	functional immunogens to elicit recognising antibodies, or antigens	237	ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg	256
CC	capable of binding antibodies. A combination, e.g., including a DCRS can			
CC	be used as an immunogen for the production of antisera or antibodies	979	ACAGCTCTGGTTCCTGCTGCTCTGCATTCAGGTGGTGGCTAGAGCCAGACTCTGAGAGG	1038
CC	capable of distinguishing between other cytokine receptor family members.			
CC	A purified DCRS can also be used as a reagent to detect antibodies	257	ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisLeu	276
CC	generated in response to the presence of elevated levels of expression,			
CC	or immunological disorders which lead to antibody production to the	1039	GTCGAATTCGTCCCTTCCTCGGGAAGATCCCGGTGCACACAGGAACCTCTTGACATAGCC	1098
CC	endogenous receptor. This sequence represents cDNA encoding the mouse			
CC	DCRS7 polypeptide	277	ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGly	296
XX				
SQ	Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 U; 0 Other;	1099	AGGCTGCGGGTACTGTCTCCAGGGGTATGGCAGCTAGATGGCTTGTGTCTGCTCGCGGC	1158
	Alignment Scores:	297	LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro	316
	Pred. No.:			
	Score:	1,298-250	Length:	2314
	3565.00	Matches:		671
	Percent Similarity:	96.3%	Conservative:	1
	Best Local Similarity:	96.1%	Mismatches:	2
	Query Match:	98.9%	Indels:	24
		6	Gaps:	1
	US-10-719-202-2 (1-674) x AAS18132 (1-2314)			
QY	1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20		
Db	199 ATGCTGTGCTCTGGTTCCTGCTGCTTGGCACTGGGCGGAACCTGTGCTCTCT	258		
QY	21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40		
Db	259 CTGGAGAGACTGATGAGGCTCAGGACATGACACGTGCTCTCTAGGCCCTCTCTCC	318		
QY	41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60		
Db	319 CTCCTGGATGGTACGTGCTCTGCTGCTGGAGCTCCAGTCTGCCAGGCCCTGTG	378		
QY	61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80		
Db	379 CTAGTGCCTACCGCTCGCAGACGGAGCTGGTGTGAGGTGTCCACAGAAGACAGATTGC	438		
QY	81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100		
Db	439 GCCCTGTGTGCTGTGGTGGTCCACTTGGCCGTGCATGGGACCTGGGCAGAGCTGAA	498		
QY	101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln	120		
Db	499 GAAGCTGGAAAGTCTGATTTCAGAACTCCAGGAGTCTAGGAAGCCCTCTCTCCAGGCC	558		
QY	121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGlnVal	140		
Db	559 GTGGTGTCTCTCTCCAGGCTTACCCCATCGCCCGCTGTGCTGCTGGAGGTCCAGGTG	618		

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Db 1699 CTCCTCCACTCCGCGCAGCGGCTACGAGCGCTGGTGAGCACTGGCGTCCGG 1758
Qy 497 LeuSerGlnMetProLeuArgValAlaValAapLeuTrpSerArgGluLeuSerAla 516
Db 1759 TTGAGCCAGATGCCACTGCGCGTGGCGGGACCTGTGGAGCGCGCGAGCTGAGCGG 1818
Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgileLeuGlnGluGlyVal 536
Db 1819 CAGGAGCCCTAGCCTGTTCCACCACGAGCGCGATCTCTGAGGAGGGTGGCGTG 1878
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeu 556
Db 1879 GTAATCCTTCTCTCTCCGCGCGCGTGGCGCGAGTGTACGAGTGGCTGCAGTCCAG 1938
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAap 576
Db 1939 ACAGTGGAGCCGCGCGCGATGACGCGCTGCGCGCTGGCTGAGCTGCTACCCGAT 1998
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValGlyPheAspGlyLeuLeuHis 596
Db 1999 TTCCTGCAAGCGCGGCGACCGCGCTACGTGGGGTCTACTTCGACGGGTGCTGCAC 2058
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTCCTCCCGTTCGCGTGGCGCGCTCTCTCTCCCTGCGCTCGCAGCTG 2118
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAap 636
Db 2119 CCGGCTTTCTCTGGATGCACTGCAGGAGAGCTCTCCACTTCGCGGGCGAGCCCGGAC 2178
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAapSerCysThrSerSerSer 656
Db 2179 CGGCTGGACAGTGAACCCAGCGCTGCGGTGCGCTCGCCCTGGACAGCTGTACTTCTAGCTCG 2238
Qy 657 GluAlaProGlyCysGluGluTrpAapLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAAGCCCCAGGCTGCTGCGAGGAATGGACCTGGGACCCCTGCACTACACTAGAA 2292

RESULT 6
ID AEB55651 standard; cDNA; 2314 BP.
XX AEB55651;
AC AEB55651;
DT 22-SEP-2005 (first entry)
DE Mouse DCSR7 polypeptide encoding cDNA.
KW Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
KW DCSR7; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
KW interstitial lung disorder; asthma; allergy; atherosclerosis;
KW gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
KW antipsoriatic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
KW antiulcer; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
KW IL-17C agonist; mouse; DCSR7; gene; s8; antisense therapy; RNAi therapy.
XX Mus musculus.
OS
XX
FH Key Location/Qualifiers
FT CDS 199..2295
FT /*tag= C
FT /product= "DCSR7"
FT mat_peptide 199..2292
FT /*tag= b
FT sig_peptide 199..258
FT /*tag= a
XX
PN WO2005065711-A2.
XX
XX 21-JUL-2005.
XX
XX 22-DEC-2004; 2004WO-US042935.

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XX 29-DEC-2003; 2003US-00749144.
PR (SCHE ) SCHERING CORP.
XX
XX Gorman DM;
PI
XX
XX WPI; 2005-506792/51.
DR P-PSDB; AEB55652.
XX
XX Modulating activity of cell, involves contacting cell with an agonist or
PT antagonist of DNAX cytokine receptor subunit.
XX
XX Example 5; SEQ ID NO 7; 130pp; English.
XX
XX The invention relates to modulating (M1) activity of cell, by contacting
CC cell with an agonist or antagonist of DNAX cytokine receptor subunit
CC (DCSR9) or of interleukin (IL)-17C where the cell modulates psoriasis,
CC inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
CC allergy, or atherosclerosis. Also provided are methods for treating (M2)
CC the disorders which involves administration of the modulator and
CC diagnosing (M3) a disorder as mentioned above that involves contacting a
CC sample from a test subject with a binding composition that specifically
CC binds to a polypeptide or nucleic acid of DCSR9 or IL-17C. (M1) is useful
CC for modulating an activity of a cell. (M2) is useful for treating a
CC subject suffering from a disorder such as psoriasis, IBD, interstitial
CC lung disorder, asthma or allergy, or atherosclerosis, where the
CC interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic
CC granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or
CC ulcerative colitis. The present sequence represents a mouse DCSR7
CC polypeptide encoding cDNA.
XX
XX SQ Sequence 2314 BP; 411 A; 725 C; 705 G; 473 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.29e-250 Length: 2314
XX Score: 3565.00 Matches: 671
XX Percent Similarity: 96.3% Conservative: 1
XX Best Local Similarity: 96.1% Mismatches: 2
XX Query Match: 98.9% Indels: 24
XX DB: 14 Gaps: 1
XX
XX US-719-202-2 (1-674) x AEB55651 (1-2314)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 199 ATGCTGTGTCTCTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 258
Qy 21 LeuGluArgLeuMetGluProGlnAapThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 259 CTGGAGAGACTGATGGAGGCTCAGGACACTGCACGCTGTCTCTAGGCTCTCTCTGCCAC 318
Qy 41 LeuTrpAapGlyAapValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 319 CTCCTGGATGGTACGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAapCys 80
Db 379 CTAGTGCCTTACCCGCTGCAGAGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 439 GCCCTCTGTGTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
Qy 101 GluAlaGlyLysSerAapSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln 120
Db 499 GAAGCTGGAAGTCTGATTTCAGAACTCCAGGAGTCTTAGGAACGCTCTCTCCAGGCCAG 558
Qy 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGlnVal 140
Db 559 GTGGTGTCTCTCTCCAGGCTTACCCATCGCCCGCTGTGCTGTGTGTGTGTGTGTGTGT 618
Qy 141 ProAlaAapLeuValGlnProGlyGlnSerValGlySerAlaValPheAapCysPheGlu 160

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Db 619 CCCGCTGACCTGGGTGAGCCCTGGCTCAGTCCGTGGGTTCTCGGGTATTGACTGTTTCGAG 678
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 679 GCTAGTCTTGGGGCTGAGGTACAGATCTGGTCTTACACGAAAGCCAGGTACAGAAAGAG 738
Qy 181 LeuAenLeuThrGlnGlnLeuPro----- 188
Db 739 CTCAACTCACACAGCAGCTGCCTGACTGCAGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
Qy 189 -----AspGlyAspAenValLeuLeuThr 196
Db 799 AGCTGCTGGGTCTGGCCCTGGCTCAATGTGTCTACAGATGTTGACAAATGCTCTTCTGACA 858
Qy 197 LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 859 CTGGATGTCTCTGAGGAGCAGGACTTTAGCTTCTTACTGTACCTGGCTGCGTCCAGTCCCGGAT 918
Qy 217 AlaLeuLysSerLeuTyrTyrLysAenLeuThrGlyProGlnAenIleThrLeuAenHis 236
Db 919 GCTCTCAATCTTGTGTGACAAACCTGACTGGACCTCAGAACATTACTTTAAACACAC 978
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
Db 979 ACAGACCTGGTTCCTCGCTCTGCATTCAGGTGTGGTCTGTAGGCCAGACTCTGAGAGG 1038
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAenLeuTrpHisIleAla 276
Db 1039 GTCGAATCTGCCCCCTTCGGGAGAGATCCCGGTGCACACAGGAACCTCTGGCACATAGCC 1098
Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysLeuProGly 296
Db 1099 AGGCTGCGGGTACTGTCCCAAGGGGTATGGCAGCTAGATGGCCTGTCTGTCTGCGGGC 1158
Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 1159 AAGGTAACTGTGTGGCAGGACACACACAGAGTCTCTGCCAGCCACTTGTGCCACCA 1218
Qy 317 ValProGlnLysAenAlaThrValAenGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1219 GTGCCCCAGAGAACGCCACTGTGAATGAGCCACCAAGATTTCCAGTTGTGTGGCAGGCCAC 1278
Qy 337 ProAenLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1279 CCCAACCTCTGTGTCCAGGTAGCACCTGGAGAGGTTACGCTCAAGCGGTGTGTGG 1338
Qy 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1339 GCTGACTCTTGGGCCCCCTTCAAGCATGATATGCTGTGTAGTGGAGATGAAAAACCGGCTC 1398
Qy 377 AenAenThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1399 AACACACATCAGTCTGTGCCTTGGAAACCCAGTGGCTGTACACCACTGCCACGATGGCC 1458
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1459 TCCACGAGAGCTGTGCTGGGAGGAGGTGTCTGCAAGACTTCGATACACACAGGTGT 1518
Qy 417 MetGlnLeuTrpAenAspAenMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
Db 1519 ATGCAGCTGTGGAACGATGACAACTGGATCGCTATGGCCCTGCCCATGACAAAGTAC 1578
Qy 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
Db 1579 ATCCACAGCGCTGGGTCTCTAGTATGGCTGGCTGCTACTCTTGGCTGCGGCGCTTTTC 1638
Qy 457 PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1639 TTCCTTCTCTTAAAGAGACCGCAGGAAGCGGCCGCTGGCTTCCCGCACGCGCTTG 1698
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496

Db 1699 CTCCTCCACTCCGCGCAGGAGCGGGCTACGAGCGCCTGGTGGGAGCACCTGGCGTCCGCG 1758
Qy 497 LeuSerGlnMetProLeuArgValAlaValAlaAspLeuTrpSerArgArgGluLeuSerAla 516
Db 1759 TTGAGCCAGATGCCACTCGCGTGGCGTGGACCTGTGTGGAGCCGCGAGCTGAGCGCG 1818
Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgGileLeuGlnGluGlyVal 536
Db 1819 CACGAGCCCTAGCTGTGTTCCACACACGAGGACGCCGTATCTCTGACAGAGGGTGGCGTG 1878
Qy 537 VallleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db 1879 GTAATCTTCTTCTGCGCCCGCGCGCTGGCGAGTGTACAGCAGTGGCTGCGAGTCCAG 1938
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
Db 1939 ACAGTGGAGCCCGGGCGCATGACGCCCTCGCGCCTGGCTGAGTGTGCTACCCGAT 1998
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1999 TTCTGCAAGCCCGGGGACCGCGCTACGTGGGGTCTACTTCGACGGGCTGTGCAC 2058
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTGCCCTCGCTTCGCGTTCGCGCCCGCTCTTCTCCCTGCGCTCGAGCTG 2118
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 2119 CCGGCTTTCCTGGAGTGCACCTGCAGGAGGCTGCTCCACTTCGCGGGGCGACCCCGGAC 2178
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 2179 CGGGTGGAAACAGTGCACCCAGCGCTGCGGTCCGCTCGGACAGCTGTACTTCTAGCTCG 2238
Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAAGCCCCAGGCTGTGCGAGGAATGGGACCTGGGACCTGCACCTACACTAGAA 2292
RESULT 7
ABL34982
ID ABL34982 standard; cDNA; 2128 BP.
XX
AC ABL34982;
XX
XX 04-APR-2002 (first entry)
DE Murine cDNA isolated from skin cells SEQ ID NO: 487.
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW ss.
XX Mus sp.
XX WO200190357-A1.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-NZ0000099.
XX
XX 24-MAY-2000; 2000US-0206650P.
PR 25-JUL-2000; 2000US-0221232P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
PI Watson JD, Strachan I, Sleeman M, Onrust R, Murison JG;
PI Kumble KD;
XX
XX WPI; 2002-122020/16.
XX
PT New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,


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QY 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1801 TTCTGCAAGCCGCGGACCGCGCTACCTCGGGGTCTACTTCGACGGGCTGTCGAC 1860

QY 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 1861 CCAGACTGTGGCCCTCCCGGTCCGGCTCGCCCGCTCTCTCCCTGCGGCTGCGAGCTG 1920

QY 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 1921 CCGGCTTCCTGGATGCACTGACGGAGGCTGCTCCACTTCGCGGGCGACCCGCGGAC 1980

QY 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 1981 CCGGTGGAACAGTACACCGCGCTGCGGTCCGCTCGGACAGCTGTACTTCTACCTCG 2040

QY 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2041 GAAGCCCCAGGCTGCTGCGAGATGGGACCTGGGACCTGCACACTACACTAGAA 2094

RESULT 8
ABK86568
ID ABK86568 standard; cDNA; 2331 BP.
AC ABK86568;
XX
XX
XX 24-SEP-2002 (first entry)
XX
XX Mouse interleukin 17 receptor like protein, IL-17RL, full length cDNA.
XX
XX Mouse; ss; gene; Interleukin 17 receptor-like protein; IL-17RL;
KW chondroileukin; bone degradation; cartilage degradation; gene therapy;
KW chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW allergic skin immune response; organ transplant rejection; cytokine;
KW osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
KW seronegative spondyloarthropathy; bone morphogenetic protein.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH 199. .2295
CDS /*tag= a
FT /product= "IL-17RL"
FT /transl_except= (pos:2077. .2079,aa:Xaa)
FT /transl_except= (pos:2161. .2163,aa:Xaa)
FT /transl_except= (pos:2200. .2202,aa:Xaa)
FT /transl_except= (pos:2242. .2244,aa:Xaa)
FT /note= "Xaa is unknown"
XX
XX WO200238764-A2.
XX
XX 16-MAY-2002.
XX
XX 13-NOV-2001; 2001WO-US043855.
XX
XX 10-NOV-2000; 2000US-0247134P.
XX 23-FEB-2001; 2001US-0271197P.
XX 12-OCT-2001; 2001US-0328904P.
XX
XX (REG ) UNIV CALIFORNIA.
XX
XX Haudenschild D, Rose L, Moseley T, Reddi AH;
XX
XX WPI; 2002-508211/54.
XX P-PSDB; AAU99161.
XX
XX Interleukin-17 receptor-like polypeptide useful for the manufacture of a
XX medicament to modulate cartilage or bone growth in a mammal.
XX
XX Claim 84; Page 88-89; 108pp; English.
XX
XX The invention relates to an interleukin-17 receptor-like (IL-17RL)
XX
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CC polypeptide, with 85% or greater sequence identity to a polypeptide with
CC a sequence appearing as AAU98781-AAU98792, where IL-17RL binds to an IL-
CC 17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F. Also included
CC are IL-17RL polynucleotides, antibodies, expression cassettes, transgenic
CC host cells, a method of determining the aggressiveness of a prostate
CC cancer cell, by determining the presence or absence in the cell of a
CC group of IL-17RL (where the determination that the group is absent in the
CC cell indicates that the cancer is more aggressive than a like cell in
CC which the group is present) and a mammalian cell comprising a
CC polynucleotide encoding an IL-17B antagonist, where the cell is selected
CC from chondrocyte, synovioocyte, and mesenchymal stem cell. IL-17RL or the
CC polynucleotide is useful for the manufacture of a medicament to modulate
CC cartilage or bone growth in a mammal. The polynucleotide is useful for
CC the manufacture of a medicament to restore androgen-responsiveness to a
CC prostate cancer cell. IL-17RL is useful for decreasing catabolic activity
CC in bone or cartilage in a mammal. IL-17RL is useful for inhibiting
CC ossification or calcification in a mammal suffering from pathological
CC ossification or calcification, for diagnosing a cartilage degenerative
CC disorder in a mammal, for inhibiting the rate of proteoglycan synthesis
CC by a chondrocyte in culture, and for the manufacture of a medicament to
CC potentiate the activity of a bone morphogenetic protein in a mammal. An
CC IL-17RL antagonist is useful for treating a bone or cartilage pathology
CC such as a degenerative cartilage disorder selected from osteoarthritis,
CC rheumatoid arthritis, relapsing polychondritis, allergic skin immune response
CC spondyloarthropathies, multiple sclerosis, and organ transplant rejection. IL-17RL is particularly a receptor for IL
CC -17B (chondroileukin, a proinflammatory cytokine). The gene for IL-17RL is
CC located on chromosome 3p25.3-3p24.1. The present sequence is the full
CC length cDNA sequence for mouse IL-17RL
XX
XX Sequence 2331 BP; 428 A; 725 C; 695 G; 473 T; 0 U; 10 Other;
SQ
Alignment Scores:
Pred. No.: 1,03e-248 Length: 2331
Score: 3539.00 Matches: 666
Percent Similarity: 95.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 7
Query Match: 98.2% Indels: 24
DB: Gaps: 1

US-10-719-202-2 (1-674) x ABK86568 (1-2331)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 199 ATGCCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 259 CTGGAGAGACTGATGGAGCCTCAGGACACTGACACCTGCTCTCTAGGCTCTCTCTGCCAC 318
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 319 CTCTGGGATGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIysThrAspCys 80
Db 379 CTAGTGCTTACCGGCTGCAGACGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 438
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 439 GCCCTGTGTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
QY 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 499 GAAGCTGGAAGCTGTGATTTCAGAACTCCAGGAGTCTAGGACGCTCTCTCCAGGCCAG 558
QY 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 559 GTGGTGCTCTCTCTCCAGGCTTACCCATCGGCCGCTGTGTGTGTGTGTGTGTGTGTGT 618
QY 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 619 CCGCTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 678
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Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgGlyGlnLysGlu 180
Db 679 GCTAGTCTTGCGGCTGAGGTACAGATCTGGTCTTACACCAAGCCAGGTACCAAGAGAG 738
Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 739 CTCAACTCTACACAGCAGCTCCCTGACTGTCAGGGGGTCTTGAAGTCCGGGACAGCATCCAG 798
Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 799 AGCTGCTGGGTCTGCTCCCTGGCTCAATGTGTCTACAGATGGTGACATGTCTCTGACA 858
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 859 CTGATGATCTCTGAGGACGAGACTTTAGCTTCTTACTGTACCTGCGTCCAGTCCCGGAT 918
Qy 217 AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 919 GCTCTCAAAATCTTGTGTGACAAAACCTGACTGGACCTCAGAAACNTTACTTTAAACCCAC 978
Qy 237 ThrAspLeuValProCysLeuCyseileGlnValTrpSerLeuGluProAspSerGluArg 256
Db 979 ACAGACTGTCTCCCTGCTGCAATTCAGGTGTGTGCTAGAGCCAGACTCTGAGAGG 1038
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAla 276
Db 1039 GTCGAATTCCTGCCCTTCCGGGAAGATCCGGGTGCACACAGGAACCTCTGGCACAATAGCC 1098
Qy 277 ArgLeuArgValLeuSerProGlyValTrpClnLeuAspAlaProCysCysLeuProGly 296
Db 1099 AGGCTGCGGGTACTGTCCCCAGGGGTATGGCAGCTAGATGGCTTGTCTGTCCCGGC 1158
Qy 297 LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 1159 AAGGTACACTGTCTGGCAGGACACAGACAGAGTCCCTGCCAGCCACTTGTGGCACCA 1218
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1219 GTGCCCCAGAAAGACGCCACTGTGAATGAGCCACAGATTTCCAGATTGGTGGCAGGCCAC 1278
Qy 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp 356
Db 1279 CCCAACTCTGTGTCCAGGTGAGCACCTGGGAGAAGGTTTCAGTGTGCAAGGCTGTGTGG 1338
Qy 357 AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu 376
Db 1339 GCTGACTCTTGGGCCCCCTTCAAGGATGATGCTGTTAGTGGAGATGAATAACCCGGCTC 1398
Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1399 AACCAACATCAGTCTGTGCTTGGNAACCCAGTGGCTGTACACCCTGCCAGCATGGCC 1458
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1459 TCCACGAGAGTGTCTGCTGGGAGAGAGTGTGTCGAAGACTTCCGATCACACCACTGT 1518
Qy 417 MetGlnLeuTrpAsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyr 436
Db 1519 ATGCAGCTGTGGAAACGATGACAAATGGATGCGTATGGGCTGCCCCATGGACAAGTAC 1578
Qy 437 IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhe 456
Db 1579 ATCCACAGCGCTGGGTCTTAGTATGCTGGCTGCTCTCTTGGCTGGCGCTTTTC 1638
Qy 457 PhePheLeuLeuLeuLysLysAspArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1639 TTCTTCTCTCTTCAAAAAGGACCGCAGGAAGCGGCTGGCTCCCGCAGCGCTTG 1698
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1699 CTCTCCACTCCGCGCAGGAGCGGGCTACAGCGCTGTGGGAGCAGCTGGGCTCCGG 1758

Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGluLeuSerAla 516
Db 1759 TTGAGCCAGATGCCACTGCGCGTGGCGTGGACCTGTGGAGCCGCCGAGCTGAGGCG 1818
Qy 517 HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgIleLeuGlnGluGlyVal 536
Db 1819 CACGAGCCCTAGCTGTGTTCACACAGCAGCGGTATCTTCAGAGAGGGTGGCGTG 1878
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln 556
Db 1879 GTAATCTCTCTCTCGCCCGCGCGTGGCGAGTGTTCAGCAGTGGCTGCAGCTCCAG 1938
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysValLeuProAsp 576
Db 1939 ACAGTGGAGCCCGCGCGCATGACGCCCTCGCGCTGGCTGCTGCTGCTGCTGCTGCTG 1998
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuHis 596
Db 1999 TTCCTGCAAGCCCGCGCGACCGCGCGCTACGTGGGGTCTACTTCGACGGGCTCTGCAC 2058
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 2059 CCAGACTCTGTGCTCCCTCCSSTTCCGGGTGCGCGGTCTTCTCTCCCTGCGCTGCGAG 2118
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 2119 CCGGCTTCTCGATGCACTGCAGGAGGCTGCTCCACTTCCCGGGGCGACCCGCGGAC 2178
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSer 656
Db 2179 CGGGTGGAAACAGTGAACCCAGSCCTGCGGTGCCCTGACACAGCTGTACTTCTAGCTCG 2238
Qy 657 GluAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu 674
Db 2239 GAASCCCGAGCTGCTGCGAGGATGGAGCTGGACCTGGACCTGCATACACTAGAA 2292

RESULT 9
AAD24221
ID AAD24221 standard; DNA; 2022 BP.
XX AC AAD24221;
XX DT 17-MAY-2002 (first entry)
XX DE Murine cytokine receptor, Zcytor14 degenerate DNA.
XX KW Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
XX KW gene therapy; protein therapy; ds.
XX OS Mus sp.
XX PN WO200204519-A2.
XX PD 17-JAN-2002.
XX PF 05-JUL-2001; 2001WO-US021344.
XX PR 06-JUL-2000; 2000US-0216446P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Gao Z;
XX PI PI
XX DR WPI; 2002-179701/23.
XX PT New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
XX PT receptor, useful for treating inflammation, specifically rheumatoid
XX PT arthritis, and as educational tools or in research.
XX PS Claim 8; Page 92; 99pp; English.
XX CC The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
XX CC polypeptide is useful for identifying or isolating Zcytor14 ligands, in

CC preparing antibodies, in identifying proteins or peptide cleavage sites,
CC in amino acid sequence analysis, and in monitoring biological activities
CC of both the native and tagged protein in vitro or in vivo. Polypeptides
CC having Zeytor14 activity can be used to treat inflammation, such as
CC rheumatoid arthritis. Zeytor14 polynucleotide may be used as educational
CC tool in genetics, molecular biology, protein chemistry and antibody
CC production analysis, in the preparation of expression constructs for
CC bacterial, viral or mammalian expression, in determining mRNA and DNA
CC localisation of Zeytor14 polynucleotide in tissues, for identifying
CC related polynucleotides and polypeptides by nucleic acid hybridisation,
CC in linkage-based testing for various diseases in murine models, and to
CC determine whether a subject's chromosomes contain a mutation in the
CC Zeytor14 gene. Zeytor14 oligonucleotide probes are useful for in vivo
CC diagnosis, and for detecting and localising Zeytor14 gene expression in
CC tissue samples. The present sequence is a degenerate form of DNA encoding
CC murine cytokine receptor, Zeytor14 (AAE14559)
XX
SQ Sequence 2022 BP; 240 A; 248 C; 377 G; 272 T; 0 U; 885 Other;

Alignment Scores:
Pred. No.: 5,286-185 Length: 2022
Score: 2666.00 Matches: 484
Percent Similarity: 71.8% Conservative: 0
Best Local Similarity: 71.8% Mismatches: 190
Query Match: 74.0% Indels: 0
DB: 6 Gaps: 0

US-10-719-202-2 (1-674) x AAD24221 (1-2022)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 1 ATGCCGNTGWSNTGGTYYTYNTYNTGNSYNTGNGNGMGAAYCCGNTGNTGNTGNSN 60
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 61 YTGARGMGNTYATGARGCNCARGAYACGNCMGNTGYWSYNTGNGYNTGNSYNTGAY 120
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTTGGGAGGNGAYGTNTYNTGYTNCNGGNSYNTYTCARWSNGCNCNGCNGCNGT 180
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 YTTGNTCCNACNMGNTYTCARACNGARYTNGTNTGNTGNTGNTGNTGNTGNTGNTG 240
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 241 GCNTYTMGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 300
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GARGCNGNAARWSNGAYWSNGARYTTCARARGWSNMGNAAYGCNWSNTYTCARACNCAR 360
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 361 GTNGTNTYNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 420
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlnSerAlaValPheAspCysPheGlu 160
Db 421 CCNCGNGAYTNGTNCARCCNGCNCARWSNGTNGNSGNCNGTNTTYGATGYTGYGAR 480
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCNWSNTYTCARACNCARGTNCARATHFGGWSNTAYACNARCCNMGNTAYCABAARGAR 540
Qy 181 LeuAsnLeuThrGlnGlnLeuProAspGlyAspAsnValLeuLeuThrLeuAspValSer 200
Db 541 YTNAAAYTNA CNCAFCARYTNCNGAYGNGAYAAAGTNTYNTYNTACNTYNTGAYTWSN 600
Qy 201 GluGlnGlnAspPheSerPheLeuLeuTyrLeuArgProValProAspAlaLeuLysSer 220
Db 601 GARGARGCARGAYTYYTWSNTTYNTYNTYNTYNTYNTGNCNGCNGTNCNGAYGCNTYTAARWSN 660

Qy 221 LeuTrpTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuVal 240
Db 661 YTTGCTAYAAARAYTTNACNGCNCARAAAYATHACNTYTAAYCAVACANGAYTNGTN 720
Qy 241 ProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheCys 260
Db 721 CCNTGYTNTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 261 ProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHisIleAlaArgLeuVal 280
Db 781 CCNTTVMGNGARGAYCCNGCNGCAYMGNAAYTNTGTCAYATGTCNMGNTYTMGNGTN 840
Qy 281 LeuSerProGlyValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeu 300
Db 841 YTMWSNCCNGGNTGTCARATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 301 CysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProValProGlnLys 320
Db 901 TGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNTYNTGTCNCCNGTNCNCARAA 960
Qy 321 AsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCys 340
Db 961 AAYGCNACNTNAAAYGARGCNCARGAYTTCARATGATGATGATGATGATGATGATGAT 1020
Qy 341 ValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeu 360
Db 1021 GTNCARGTWSNACNTGGGARAARGTNCARATGATGATGATGATGATGATGATGATGAT 1080
Qy 361 GlyProPheLysAspAspMetLeuLeuValGluMetLysThrGlyLeuAsnThrSer 380
Db 1081 GCNCCNTTYAARGAYATGYTNTGNTGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 381 ValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla 400
Db 1141 GTNTGYGNTGARGCNCWSNGGNTGYACCCNTYTCNWSNATGCGNWSNACNMGNGCN 1200
Qy 401 AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrp 420
Db 1201 GCNMGNTYTCARGARGAYTNTYTCARGAYTYTMGNSNCAICARTGATGATGATGATG 1260
Qy 421 AsnAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTyrIleHisArgArg 440
Db 1261 AAYGAYGAYAAAYATGGGWSNTYTTGGCNGTGYCCNATGGAYAAATATATCAVMGNGN 1320
Qy 441 TrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPhePhePheLeuLeu 460
Db 1321 TGGTNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNT 1380
Qy 461 LeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeuLeuHisSer 480
Db 1381 YTNAAARARGAYMGNGNAARCCNCGNMGNGNMGNMGNMGNMGNMGNMGNMGNMGNMG 1440
Qy 481 AlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMet 500
Db 1441 GCNGAYGNGCNGGNTATGARGMNTGNTGNGCNGTNGCNGCNGCNGCNGCNGCNGCNG 1500
Qy 501 ProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAlaHisGlyAlaLeu 520
Db 1501 CCNTYTMGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTG 1560
Qy 521 AlaTrpPheHisGlnArgArgGlyLeuGlnGluGlyGlyValValValLeuLeu 540
Db 1561 GCNTGTTTCAYCAYCARMGNGMGNATHYTNCARGARGGNGGNTGNTGNTGNTGNTGNT 1620
Qy 541 PheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro 560
Db 1621 TTWSNCCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 1680
Qy 561 GlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAspPheLeuGlnGly 580
Db 1681 GGNCCNCAAYGCNTGNGCNGCNGTGGTYTWSNTGTYTNTGNTGNTGNTGNTGNTGNTG 1740
Qy 581 ArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVal 600

Db 1741 MGNCGNACNGMNTAYGTNGGNGTNTATYTYGAYGNTYNTNCAAYCCNGAYWSNGTN 1800
 Qy 601 ProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeu 620
 Db 1801 CCWNSCCTTYMGNGTNGCNGCTYNTTYSNTNCCNACNARYTNCNGCNGNTTYTN 1860
 Qy 621 AspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArg 640
 Db 1861 GAYCNYTNCARGGNGNTGYWSNACWNSGNGCNGNGCNGCNGAYMGNGTNGARMGN 1920
 Qy 641 ValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaProGly 660
 Db 1921 GTNACNARGCNYTNGMNGCNGTNGAYWSNTGYACWNSWNSGNGCNGCNGGNG 1980
 Qy 661 CysCysGluGluTTPAspLeuGlyProCysThrThrLeuGlu 674
 Db 1981 TGYTGARGARTGGGAYTNGGNCCTGYACNACNTNGAR 2022

RESULT 10
 ID AAD24223 standard; DNA; 2094 BP.
 XX AAD24223;
 AC AAD24223;
 XX 17-MAY-2002 (first entry)
 XX Murine Zcytor14 cytokine receptor variant, Zcytor14-1 degenerate DNA.
 DE Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
 KW gene therapy; protein therapy; Zcytor14-1; ds.
 KW
 XX Mus sp.
 XX W0200204519-A2.
 FN
 XX 17-JAN-2002.
 PD
 XX 05-JUL-2001; 2001WO-US021344.
 PF
 XX 06-JUL-2000; 2000US-0216446P.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Gao Z;
 XX WPI; 2002-179701/23.
 DR
 XX New murine cytokine receptor, Zcytor14, and polynucleotides encoding the
 PT receptor, useful for treating inflammation, specifically rheumatoid
 PT arthritis, and as educational tools or in research.
 XX
 PS Claim 8; Page 97-98; 99pp; English.
 XX
 CC The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14
 CC polypeptide is useful for identifying or isolating Zcytor14 ligands in
 CC preparing antibodies, in identifying proteins or peptide cleavage sites,
 CC in amino acid sequence analysis, and in monitoring biological activities
 CC of both the native and tagged protein in vitro or in vivo. Polypeptides
 CC having Zcytor14 activity can be used to treat inflammation, such as
 CC rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational
 CC tool in genetics, molecular biology, protein chemistry and antibody
 CC production analysis, in the preparation of expression constructs for
 CC bacterial, viral or mammalian expression, in determining mRNA and DNA
 CC localisation of Zcytor14 polynucleotide in tissues, for identifying
 CC related polynucleotides and polypeptides by nucleic acid hybridisation,
 CC in linkage-based testing for various diseases in murine models, and to
 CC determine whether a subject's chromosomes contain a mutation in the
 CC Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo
 CC diagnosis, and for detecting and localising Zcytor14 gene expression in
 CC tissue samples. The present sequence is a degenerate form of DNA encoding
 CC murine Zcytor14 variant, Zcytor14-1 (AAE14560)

SQ Sequence 2094 BP; 248 A; 252 C; 393 G; 283 T; 0 U; 918 Other;
 Alignment Scores:
 Pred. No.: 2,23e-183 Length: 2094
 Score: 2644.00 Matches: 484
 Percent Similarity: 69.3% Conservative: 0
 Best Local Similarity: 69.3% Mismatches: 190
 Query Match: 73.3% Indels: 24
 DB: 6 Gaps: 1

US-10-719-202-2 (1-674) x AAD24223 (1-2094)

Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAenProValValValSer 20
 Db 1 ATGCCNGTWSNTGGTYYTYNTYNTWSYNTGCTYNTGNGMGNAAAYCCNGTNGTNGTWSN 60
 Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
 Db 61 YTNGARMGNYTNAATGGARCCNCARGAYACNGCMNGTGYWSNTYNTGNGNYTNWSNTGYCAY 120
 Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
 Db 121 YTNNGGAYGGNGAYGTNTYNTGTYTNCNGGWSNYTNCARWSNCCNGCNGCNGT 180
 Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
 Db 181 YTNGTTCNCCNACMGNTYTCARACNCGARYTNGTYNTMGNTGYCCNCAARAACNGAYTG 240
 Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
 Db 241 GCNYTNMGNGTNGMNGTNGTNCAYTYTNGCNGTNCAYGNGCAYTGGGCGARGCCNGAR 300
 Qy 101 GluAlaGlySerSerAspSerGluLeuGlnGluSerArgAenAlaSerLeuGlnAlaGln 120
 Db 301 GARGCNGNAARWSNGAYWSNGARYTNCARGARWSNMGNAAAYCCNWSNTYTCARGCNCAR 360
 Qy 121 ValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
 Db 361 GTNGTYNTWSNTTYCARGCNTAYCCNATHGCMNGNTGYGCNTYNTNGARGTNCARGTN 420
 Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
 Db 421 CCNGCNGAYTYTNGTNCARGCNGCARGWSNGTNGGWSNCGCTNTTYTAYTYGTYTYGAR 480
 Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyThrLysProArgTyTrpGlnLysGlu 180
 Db 481 GCNWSNTYTNNGCNGCARGTNCARATHTGGWSNTAYACNAARCCNMGNTAYCARAARGAR 540
 Qy 181 LeuAsnLeuThrGlnGlnLeuPro-----AspGlyAspAenValLeuLeuThr 196
 Db 541 YTNAAAYTNACNCAARCARYTNCNGAYTYGMNGNGNYTNGARGTNMGNGAYWSNATHCAR 600
 Qy 189 -----AspGlyAspAenValLeuLeuThr 196
 Db 601 WSNTGYTGCGTNTYNTCCNTGGYTNAAYGTNWSNACNGAYGGNGAYAAAYGTNTYNTNACN 660
 Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyTrpLeuArgProValProAsp 216
 Db 661 YTNNGAYTGNWSNGARGCARGAYTYTWSNTTYTNTTAYTYTNMGNCNGTNCNGAY 720
 Qy 217 AlaLeuLysSerLeuTrpTyLysAenLeuLeuGlyProGlnAenIleThrLeuAsnHis 236
 Db 721 GCNTYTNAAWSNTYNTGGTAYAAARAAYTYTNACNGCNCNCAARAAYATHACNTYNTAAAYCAY 780
 Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAspSerGluArg 256
 Db 781 ACNGAYTYTNGTNCCTGTYTNTGYATHCARGTNTGWSNYTNGARGCNGAYWSNGARMGN 840
 Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAenLeuTrpHisIleAla 276
 Db 841 GTNGARTTYTGCTNTYTMNGARGAYCCNGGNGCNCAYMGNAAAYTYNTGGCAYATHGCN 900
 Qy 277 ArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysLeuProGly 296

Db	1981	MGNTGNGARMGNGTGNACARGCNYTNWGNWNGCNYTNGAYWNTGYACNWSNWSN	2040
Qy	657	GlulAlaProGlyCysCysGluGluTrpAspLeuGlyProCysThrThrLeuGlu	674
Db	2041	GARGCNCNGGNTGYTGARGARTGGGAYTNGGNCNCNTGYACNACNTTNGAR	2094
Db	11	RESULT 11	
Db	AAS18133	standard; cDNA; 2094 BP.	
Db	AAS18133		
Db	26-MAR-2002	(first entry)	
Db	Mouse DCRS7 reverse translation generic cDNA.		
Db	Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling; ss;		
Db	gene therapy; protein therapy; immunological disorder.		
Db	Mus musculus.		
Db	WO200190358-A2.		
Db	29-NOV-2001.		
Db	23-MAY-2001;	2001NO-US016767.	
Db	24-MAY-2000;	2000US-0206862P.	
Db	(SCHE) SCHERING CORP.		
Db	Gorman DM;		
Db	WPI; 2002-106198/14.		
Db	Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide		
Db	useful for detecting antibodies generated in response to presence of		
Db	increased protein levels or immunological disorders.		
Db	Disclosure; Page 20-21; 148pp; English.		
Db	The invention relates to primate and rodent DNAX cytokine receptor		
Db	subunit (DCRS) polypeptides and the polynucleotides encoding them. The		
Db	receptors, or their portions may be useful as phosphate labelling enzymes		
Db	to label general or specific substrates. The subunits may also be		
Db	functional immunogens to elicit recognising antibodies, or antigens		
Db	capable of binding antibodies. A combination, e.g., including a DCRS can		
Db	be used as an immunogen for the production of antisera or antibodies		
Db	capable of distinguishing between other cytokine receptor family members.		
Db	A purified DCRS can also be used as a reagent to detect antibodies		
Db	generated in response to the presence of elevated levels of expression,		
Db	or immunological disorders which lead to antibody production to the		
Db	endogenous receptor. This sequence represents mouse DCRS7 reverse		
Db	translation generic cDNA		
Db	Sequence 2094 BP; 247 A; 251 C; 393 G; 285 T; 0 U; 918 Other;		
Db	Alignment Scores:		
Db	Prod. No.:	7,25e-183	Length: 2094
Db	Score:	2637.00	Matches: 483
Db	Percent Similarity:	69.2%	Conservative: 0
Db	Best Local Similarity:	69.2%	Mismatches: 191
Db	Query Match:	73.1%	Indels: 24
Db		6	Gaps: 1
Db	US-10-719-202-2 (1-674) x AAS18133 (1-2094)		
Qy	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20
Db	1	ATGCCGTWNSNTGGTYYTNTYNTWNSYTNNGCNYTNGGNGNAAAYCCNGTNGTNGTWSN	60
Qy	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
Db	901	MGNTYNTMGNTYNTWNSCNCNGGNTGTGCARYTNGAYCNCNCNTGYGYTNCNCNGN	960
Qy	297	LysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProPro	316
Db	961	AARGTNACNTYNTGTGGCARGCNCNGAYCARWSNCNCNTGYCARCNCYNTNGTNCNCNCN	1020
Qy	317	ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis	336
Db	1021	GTNCCNCARAAAYGCNACNGTNAAYGARCNCARGAYTTYCARYTNGTNGCNGNCAY	1080
Qy	337	ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCysSerTrp	356
Db	1081	CCNAAAYTNTGTGTCARGTWNACNTGGGARAARGTNCARYTNCARGCNCNTGWSNTGG	1140
Qy	357	AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu	376
Db	1141	GCNGAYWSNYTNGCNCNTTVAARGAYATGYTNTYNTGTNGTNGARATGAARACNGNYTN	1200
Qy	377	AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla	396
Db	1201	AAAYAYACNWSNGTNTGTGNTYTCARCNCNWSNGTGTACNCCNYTNCNWSNATGGCN	1260
Qy	397	SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys	416
Db	1261	WSNACNMGNCNCNGNYTNGGARGARYTNTNCARGAYTTYTMGNWSNCAYCARTGY	1320
Qy	417	MetGlnLeuTrpAsnAspAspMetGlySerLeuTrpAlaCysProMetAspLysTyr	436
Db	1321	ATGCARYTNTGAAAYGAYGAYATGGGNSNYTNTGGCNCNTGYCCNATGGAYARTAY	1380
Qy	437	IleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaLeuPhe	456
Db	1381	ATHCAYWNGMNTGGTNTGTNTGTGTYTNGTNTGYTNTYNTYNTGNCNGCNYTNTTY	1440
Qy	457	PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu	476
Db	1441	TTTTTYTNTYNTNAAARGAYTMGNMGARGCNCNGMNGNWSNMGNCNCNTYN	1500
Qy	477	LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla	496
Db	1501	YTYNTNCAYWSNGCNGAYGNGCNGNTAYARGMNTYNTGTNGCNCNTYTCNWSNCGN	1560
Qy	497	LeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAla	516
Db	1561	YTWNSNCARATGCNTYNTMGNTGNCNTGNTGAYTNTGWSNMGNGARGARYTNWSNCGN	1620
Qy	517	HisGlyAlaLeuAlaTrpPheHisHisGlnArgArgGlyLeuGlnGlyGlyVal	536
Db	1621	CAYGGCNCYNTGTCGTTTCAYCAYCARMNGMNGMGNATHYTCARGARGGNGGNTN	1680
Qy	537	ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeuGlnLeuGln	556
Db	1681	GTNATHYNTYNTYWSNCCNGCNGTNGCNCARTGYCARGARTGGYTNCARYTNCAR	1740
Qy	557	ThrValGluProGlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuProAsp	576
Db	1741	ACNGTNGARCCNGCNCNCAYGAYCNYTNCNCNTGGYTNWSNTGTGTYNTNCNCAY	1800
Qy	577	PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis	596
Db	1801	TTTTYNTCARGMNGMNGCNCNGMNTAYGTNGGNGTNTAYTYTGAGGNYTYNTNCAY	1860
Qy	597	ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu	616
Db	1861	CCNGAYWSNGTNCNWSNCCNTYNTMGNTGNCNCNTYNTTYTWSNYTNCNACNARYTN	1920
Qy	617	ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp	636
Db	1921	CCNGCNCNTTYTNGAYCNYTNCARGGNGTGYWSNACNWSNCGCNGMNGCNCNGCAY	1980
Qy	637	ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSer	656

Db 61 YTNAGRMGNTNATGGARCCNCCARGAYACNGCMNGNTGYWSNTYNTGGNTYNTWSNTGYCAY 120
Qy 41 LeuTTPAaspGlyAaspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 121 YTNWGGAYGGNGAYGTNTYNTGYTNCNGGWSNTYNTCARWSNGCNCNGCNGCNGTN 180
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 181 YTNGTNCNACNMGNNTNCCARACNGARYTNGTNTYNTMGNTGYCCNCARAAACNGAYTG 240
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTTPAlaGluProGlu 100
Db 241 GCNTYNTGYTNGMGTNGTNGTNCAYTNGCNGTNCAYGGNCAYTGGCNGARCCNGAR 300
Qy 101 GluAlaGlyLysSerAspSerGluLeuGlnGlnSerArgAsnAlaSerLeuGlnAlaGln 120
Db 301 GARGCNGNARWSNGAYWSNGARYTNCARGARWSNMGNAAYGCNWSNTYNTCARGCNCAR 360
Qy 121 ValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeuGluValGlnVal 140
Db 361 GTNGTNTYNTWSNTTYCARGCWTAYCCNATHGCMNGTGYGCNTYNTYNTNGARGTNCARGTN 420
Qy 141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
Db 421 CCNGCNGAYTNGTNCARCCNGCNGCARWSNGTNGGWSNCCNGTNTTYGAYTGYTYGAR 480
Qy 161 AlaSerLeuGlyAlaGluValGlnIleTyrSerTyrThrLysProArgTyrGlnLysGlu 180
Db 481 GCNWSNTYNTGCGCNGARGTNCARATHGTGWSNTAYACNAARCCNMGNTAYCARAARGAR 540
Qy 181 LeuAsnLeuThrGlnGlnLeuPro----- 188
Db 541 YTNAAAYTNCACNARCARYTNCNGAYTYGWMGNGNTYNTGARGTNGMNGAYWSNATHCAR 600
Qy 189 -----AspGlyAspAsnValLeuLeuThr 196
Db 601 WSNTGYTGGTNTYNTCCNTGGYTNAAYTGNWSNACNGAYGGNGAYAYGTNTYNTNACN 660
Qy 197 LeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeuArgProValProAsp 216
Db 661 YTNAGAYTWSNGARGARCARGAYTYYTWSNTTYTNTYNTAYTNTMGNCNGTNCNGAY 720
Qy 217 AlaLeuLysSerLeuTyrTyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis 236
Db 721 GCNTYNTAARWSNTYNTGGTAYAAARAYTTCACNGCNCARAAAYATHACNTYNTAAAYCAY 780
Qy 237 ThrAspLeuValProCysLeuCysIleGlnValTyrSerLeuGluProAspSerGluArg 256
Db 781 ACNGAYTNGTNCNTGYTNTGYATHCARGTNTGGWSNTYNTGARGCNGAYWSNGARMGN 840
Qy 257 ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTyrHisIleAla 276
Db 841 GTNGARTTYTGYCCNTTYMGNGARGAYCCNGGNGCNCAYMGNAAYTNTGGCAYATHGCN 900
Qy 277 ArgLeuArgValLeuSerProGlyValTyrGlnLeuAspAlaProCysCysLeuProGly 296
Db 901 MGNNTYNTMGNTYNTWSNCCNGGNTNGTGGCARYTNGAYGCNCCNTGYTYTNCNGCN 960
Qy 297 LysValThrLeuCysTyrGlnAlaProAspGlnSerProCysGlnProLeuValProPro 316
Db 961 AARGTNCNTYNTGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNTYNTGTNGTNCNCN 1020
Qy 317 ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis 336
Db 1021 GTNCCNCAARAAYGCNACNGTNAAYGARGCNCARGAYTTCARYTNGTNGCNGCNGAY 1080
Qy 337 ProAsnLeuCysValGlnValSerThrTyrGluLysValGlnLeuGlnAlaCysSerTyr 356
Db 1081 CCNAAAYTNTGYTNCARGTWSNACNTGGGARAARGTNCARYTNCARGCNGTYTNTGG 1140
Qy 357 AlaAspSerLeuGlyProPheLysAspAspMetLeuValGluMetLysThrGlyLeu 376
Db 1141 GCNGAYWSNTYNTGNCNCNTTYAARGAYGAYATGYTNTYNTGTNGTNGARATGAARACNGGNTN 1200

Qy 377 AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla 396
Db 1201 AAYAAACNWSNGTNTGYCNYTNGARCCNWSNGNTGYACNCCNTYNTCCNWSNATGCGN 1260
Qy 397 SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys 416
Db 1261 WSNACNMGNGCNGNMGNTYNTGNGNGARGARYTNTYNTCARGAYTTYMGNWSNCAYCARTGY 1320
Qy 417 MetGlnLeuTyrAsnAspAspAsnMetGlySerLeuTyrAlaCysProMetAspLysTyr 436
Db 1321 ATCCARYTNTGGAAAYGAYGAYATGGGWSNTYNTGGCNGTGYCCNATGGAYAAATAY 1380
Qy 437 IleHisArgArgTyrValLeuValTyrLeuAlaCysLeuLeuAlaAlaLeuPhe 456
Db 1381 ATHCAYMGNMGNTGGTNTYNTGTNGTNGCNYTNTYNTYNTGCGCNGCNGCNYTNTTY 1440
Qy 457 PhePheLeuLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu 476
Db 1441 TTYTYYTNTYNTTNAARAARGAYMGNMGNAARGCNGCNGMNGNWSNMGNACNGCNYTN 1500
Qy 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 1501 YNTYNTCAYSWNGCNGAYGGGCGNGTAYGARMGNYTNGTNGGNGCNYTNGCNGWSNCGN 1560
Qy 497 LeuSerGlnMetProLeuArgValAlaValAspLeuTyrSerArgArgGluLeuSerAla 516
Db 1561 YTNWSNCAATGCCNTYNTMGNTGCGTNGAYTNTTGGWSNMGNMGNGARYTNTWSNCGN 1620
Qy 517 HisGlyAlaLeuAlaTyrPheHisHisGlnArgArgIleLeuGlnGluGlyVal 536
Db 1621 CAYGCGCNYTNGCNTGGTTCAYCAYCARMGNGMNGNATHYNTNCARGAGCGGNGTIN 1680
Qy 537 ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTyrLeuGlnLeuGln 556
Db 1681 GTNATHYNTYNTYNTWSNCCNGCNGTNGCNCARTGYCARCTGGYTNCARYTNCAR 1740
Qy 557 ThrValGluProGlyProHisAspAlaLeuAlaAlaTyrLeuSerCysValLeuProAsp 576
Db 1741 ACNGTNGARCCNGCNCAYGAYGCGTNGCNGCNGTGGYTNTWSNTGYTNTYNTCCNGAY 1800
Qy 577 PheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeuHis 596
Db 1801 TTYTNTCARGGNGMNGCNCNGCMGNTAYGTNGCGTNTAYTTCAYGCGNYTNTNCAY 1860
Qy 597 ProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeu 616
Db 1861 CCNGAYWSNGTNCNWSNCCNTTYMGNTGNGCNCCTYNTYNTWSNTYNTCCNWSNCARYTN 1920
Qy 617 ProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAlaAsp 636
Db 1921 CCNGCNYTNTYNTGAYGCNTYNTCARGGNGGNTGYWSNACNWSNCGNMGNCNGCNGAY 1980
Qy 637 ArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSer 656
Db 1981 MNGTNGARMGNTNACNCCARGCNYTNGMWSNCGNYTNGAYWSNTGYACNWSNWSN 2040
Qy 657 GluAlaProGlyCysCysGluGluTyrAspLeuGlyProCysThrThrLeuGlu 674
Db 2041 GARGCNCNGTGYTGYGARGARTGGGAYTNGGNCCTGTGACNACNCTYNTNGAR 2094

RESULT 12

AAC85027
ID AAC85027 standard; cDNA; 2255 BP.

AC AAC85027;

XX 08-MAY-2001 (first entry)

DE Human cytokine receptor Zcytor14 encoding cDNA.

XX Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antiinflammatory; gene therapy; vaccine; ss.
KW


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Qy 448 CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys 467
Db 1531 TGCCTACTCTTGGCGCTGGCTTCCCTCATCTCTCTCAAAAGGATCAGCGGAA 1590
Qy 468 AlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGlu 487
Db 1591 GCGGCGCGCAGGCGCGCGCTGCTCTCTACTCAGCCGATGACTCGGGTTTCGAG 1650
Qy 488 ArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValAsp 507
Db 1651 CGCTGTGGCGCCCTGGGCTGGCCCTGTGCAGCTGCGCTGGCGTGGCGGTAGAC 1710
Qy 508 LeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArg 527
Db 1711 CTGTGAGCGCTGCTGAACGTAGCGCGCGAGCGCGCTGCTTGTCTCTCTCCCGTGGCGG 1770
Qy 528 ArgArgIleLeuGlnGlyGlyValValValIleLeuLeuPheSerProAlaAlaValAla 547
Db 1771 CGCCAGACCTGACAGAGGCGCGGTGTGTCTTGTCTCTCTCTCCCGTGGCGG 1830
Qy 548 GlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluPro-----GlyProHisAsp 564
Db 1831 CTGTGACGAGTGGCTACAGATGGGTGTCCGGGCGCGGCGCACGCGCCGACGAC 1890
Qy 565 AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly 584
Db 1891 GCCTTCGGCGCTCGCTCAGTCGCTGTGCTGCGGACTTCTTGAGGGCGGCGCGCGC 1950
Qy 585 ArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerProPhe 604
Db 1951 AGCTAGCTGGGGCGCTGCTTCGACAGGCTGCTCCACCGGACCGCTACCCCGCTTTTC 2010
Qy 605 ArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGln 624
Db 2011 CGCACCGTGGCGTGTTCACATGCTCCCTCCAACTGCCAGACTTCTTGGGGCGCTGCAG 2070
Qy 625 GlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAla 644
Db 2071 CAGCTCGCGCGCGCTTCCGGGGCTCCAGAGAGAGCGGAGCAAGTGTCCCGGCGC 2130
Qy 645 LeuArgSerAlaLeuAspSerCys-----ThrSerSerSerGluAlaProGly 660
Db 2131 CTTACCGACCGCTGTAGTAGTACTTCCATCCCGCGGAGCTCCCGCGCGGGA 2184

RESULT 13
AAD47894
ID AAD47894 standard; cDNA; 2255 BP.
XX
AC AAD47894;
DT
DT 12-FEB-2004 (first entry)
XX
DE Human cytokine receptor Zcytor14 cDNA.
XX
KW Cytokine receptor; Zcytor14; chromosome 3p25-3p24; cardiomyopathy;
KW xeroderma pigmentosum; Marfan-like connective tissue disorder;
KW diabetes mellitus; Fanconi anaemia; renal cell carcinoma; gene;
KW Marfan syndrome; Von Hippel-Lindau syndrome; blepharophimosis; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154..2232
FT /*tag= a
FT /product= "Zcytor14 precursor protein"
FT sig_peptide 154..213
FT /*tag= b
FT mat_peptide 214..2229
FT /*tag= c
FT /product= "Mature Zcytor14 protein"
XX
XX US2003199041-A1.

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PD 23-OCT-2003.
XX
PF 10-JUN-2003; 2003US-00458647.
XX
PR 07-JUL-1999; 99US-0142555P.
PR 30-JUN-2000; 2000US-00608918.
XX
(PRES/) PRESNELL S R.
(PA BURK/) BURKHEAD S K.
(PA POWN/) POWDER S L.
XX
Presnell SR, Burkhead SK, Powder SL;
WPI; 2003-852791/79.
DR P-PSDB; ABW01911.
XX
New zcytor14 polypeptides, useful for treating xeroderma pigmentosum,
PT Marfan-like connective tissue disorder, cardiomyopathy, diabetes
PT mellitus, Fanconi anemia, renal cell carcinoma and Marfan syndrome.
XX
Claim 8; SEQ ID NO 1; Opp; English.
XX
The invention relates to human cytokine receptor Zcytor14 polypeptide and
CC polynucleotide. The Zcytor14 gene is located on human chromosome 3p25-
CC 3p24. The Zcytor14 polypeptide, polynucleotide and antibody are useful
CC for treating xeroderma pigmentosum, Marfan-like connective tissue
CC disorder, cardiomyopathy, diabetes mellitus, Fanconi anaemia, renal cell
CC carcinoma, Marfan syndrome, Von Hippel-Lindau syndrome, or
CC blepharophimosis. The present sequence is human cytokine receptor
CC Zcytor14 cDNA
XX
SQ Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,88e-162 Length: 2255
Score: 2352.50 Matches: 457
Percent Similarity: 77.1% Conservative: 66
Best Local Similarity: 67.4% Mismatches: 136
Query Match: 65.3% Indels: 19
DB: Gaps: 5

US-10-719-202-2 (1-674) x AAD47894 (1-2255)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 154 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 214 CTGGAGAGGCTTGTGGGGCTCAGAGCGCTACCCACTGCTCTCCGGGCTCTCTGCGCG 273
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 274 CTCTGGGACAGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 334 CTGGGCGCTTACGACCTGCGAGAGCTGGTGTGCTGAGGTGCGCAGAGGACCGACTGT 393
Qy 81 AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 394 GACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
Qy 101 Glu-----AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 116
Db 454 GATGAGGAAAAGCTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCTAGGAATGCTCT 513
Qy 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 136
Db 514 CTCCAGGGCCAAAGTGTGTCTCTCTCCAGGCTTACCTTACTGCCCGCTGCGTCTGCTG 573
Qy 137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe 156

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XX (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
 PI Jaspers SR, Billeborough J;
 XX WPI; 2006-067457/07.
 DR P-PSDB; AEF05349, AEF05350.
 XX
 XX New isolated soluble receptor comprises at least one Zcytor14 subunit,
 PT useful for treating an inflammatory disease, e.g. asthma, inflammatory
 PT bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
 PT psoriasis.
 XX
 XX Example 28; SEQ ID NO 1; 205pp; English.
 XX
 CC The invention describes an isolated soluble receptor comprises at least
 CC one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
 CC comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
 CC amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
 CC ID NO. 24) given in the specification. Also described are: an isolated
 CC soluble receptor comprising Zcytor14, where Zcytor14 comprises a
 CC polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
 CC the pro-inflammatory activity of either IL-17A comprising fully defined
 CC 155 amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
 CC amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
 CC to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
 CC and where the antibody or antibody fragment reduces the pro-inflammatory
 CC activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
 CC reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
 CC afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
 CC role; and treating a pathological condition in a subject associated with
 CC Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
 CC subunit is useful for treating an inflammatory disease, e.g. asthma;
 CC chronic inflammatory disease selected from inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
 CC psoriasis; or acute inflammatory disease selected from endotoxemia,
 CC septicemia, toxic shock syndrome, or infectious disease. This sequence
 CC represents human IL-17A and IL-17F receptor zcytor14.
 XX
 SQ Sequence 2255 BP; 369 A; 748 C; 703 G; 435 T; 0 U; 0 Other;
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Alignment Scores:
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 Best Local Similarity: 67.4% Mismatches: 136
 Query Match: 65.3% Indels: 19
 DB: 15 Gaps: 5

US-10-719-202-2 (1-674) x AEF05348 (1-2255)

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 QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
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 QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
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Qy	508	LeuTrpSerArgGlnLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArg	527
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Qy	528	ArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSerProAlaValAlaVala	547
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XX	DT	18-DEC-2001 (first entry)	
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KW	KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;	
KW	KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;	
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XX	PN	WO200168848-A2.	
XX	PD	20-SEP-2001.	
XX	PF	28-FEB-2001; 2001WO-US006520.	
XX	PR	01-MAR-2000; 2000WO-US005601.	
XX	PR	02-MAR-2000; 2000WO-US005841.	
XX	PR	03-MAR-2000; 2000US-0187202P.	
XX	PR	06-MAR-2000; 2000US-0186968P.	
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XX	PR	15-MAR-2000; 2000US-0189328P.	
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us-10-719-202-2.p2n.rng

Tue Aug 22 11:34:35 2006

GenCore version 5.1.1.9
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OM protein - nucleic search, using frame_plus_p2n_model

Run on: August 17, 2006, 08:41:10 ; Search time 8883 Seconds
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3605	100.0	2153	6	AF458066 Mus muscu
2	3605	100.0	2256	2	AX360307 Sequence
3	3583	99.4	2328	2	AX360310 Sequence

4	3572.5	99.1	2269	2	CS251263	CS251263 Sequence
5	3569.5	99.0	2287	2	CS251267	CS251267 Sequence
6	3565	98.9	2314	2	CS135270	CS135270 Sequence
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11	2644	73.3	2094	2	AX360312	AX360312 Sequence
12	2637	73.1	2094	2	AX350978	AX350978 Sequence
13	2352.5	65.3	2255	2	CS251239	CS251239 Sequence
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26	2335	64.8	2350	2	AX720680	AX720680 Sequence
27	2332	64.7	2369	5	AY358840	AY358840 Homo sapi
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40	2235	62.0	2308	2	CS135268	CS135268 Sequence
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42	2222	61.6	2343	2	AX720678	AX720678 Sequence
43	2184	60.6	2314	2	AX720676	AX720676 Sequence
44	2182	60.5	2499	2	BD123623	BD123623 Secretary
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ALIGNMENTS

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DEFINITION	AF458066				
ACCESSION	AF458066.1	GI:21779859			
VERSION					
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 2153)				
AUTHORS	Gilbert, J.M. and Gorman, D.M.				
TITLE	Identification of novel IL-17 related receptors				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2153)				
AUTHORS	Gilbert, J.M. and Gorman, D.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-DEC-2001) Genomics, DNAX Research Inc., 901 California Ave., Palo Alto, CA 94304, USA				
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RESULT 2
AX360307
LOCUS AX360307 2256 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 1 from Patent WO0204519.
ACCESSION AX360307
VERSION AX360307.1 GI:18675809
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE
AUTHORS Gao, Z.
TITLE Murine cytokine receptor
JOURNAL Patent: WO 0204519-A 1 17-JAN-2002;
Zymogenetics, Inc. (US)
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ORIGIN

Alignment Scores:

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Query Match:	100.0%	Indels:	0
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US-10-719-202-2 (1-674) x AX360307 (1-2256)

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Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
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Qy 161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArgTyrGlnLysGlu 180
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DEFINITION Sequence 25 from Patent WO2005123778.
ACCESSION CS251263
VERSION CS251263.1 GI:85361024
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Presnell, S.R.
AUTHORS Soluble zcytor14, anti-zcytor14 antibodies and binding partners and
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Score: 3572.50 Matches: 671
Percent Similarity: 98.4% Conservative: 1
Best Local Similarity: 98.2% Mismatches: 2
Query Match: 99.1% Indels: 9
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US-10-719-202-2 (1-674) x CS251263 (1-2269)

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DEFINITION Sequence 29 from Patent WO2005123778.
ACCESSION CS251267
VERSION CS251267.1 GI:85361025
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ACCESSION AX350976
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REFERENCE
AUTHORS Gorman,D.M.
TITLE Mammalian receptor proteins: related reagents and methods
JOURNAL Patent: WO 0190358-A 10 29-NOV-2001;
SCHERING CORPORATION (US)
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Qy	317	ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis	336	RESULT 8		
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Qy	337	ProAsnLeuCysValGlnValSerThrTyrGluLysValGlnLeuGlnAlaCysSerTrp	356	LOCUS	AX720728	Sequence 74 from Patent WO0238764.
Db	1279	CCCAACCTCTGTCTCCAGGTGAGCACCCTGGGAGAGGTTGAGTCAAGCGCTGTGTGG	1338	DEFINITION	AX720728	AX720728.1 GI:29892514
Qy	357	AlaAspSerLeuGlyProPheLysAspAspMetLeuValGluMetLysThrGlyLeu	376	ACCESSION		
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Qy	417	MetGlnLeuTyrAsnAspAspAsnMetGlySerLeuTyrAlaCysProMetAspLysTyr	436	AUTHORS		Haudenschild,D., Rose,L., Moseley,T. and Reddi,A.H.
Db	1519	ATGACGTGTGGACAGATGACAAATGGATGCTATGGGCTGCGCCCATGGACAAATAC	1578	TITLE		IL-17 receptor-like protein, uses thereof, and modulation of
Qy	437	IleHisArgArgTyrValLeuValTyrPleuAlaCysLeuLeuLeuAlaAlaLeuPhe	456	JOURNAL		catabolic activity of il-17 cytokines on bone and cartilage
Db	1579	ATCCACAGCGCTGGTCTAGTATGGTGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCT	1638			Patent: WO 0238764-A 74 16-MAY-2002;
Qy	457	PhePheLeuLeuLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu	476	FEATURES		The Regents of the University of California (US)
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RESULT 9
BC004759
LOCUS
DEFINITION

BC004759 2015 bp mRNA linear ROD 03-OCT-2003
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IMAGE:3154616), complete cds.

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QY 617 ProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAsp 636
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Tue Aug 22 11:34:34 2006

ACCESSION	BC004759	BC004759.1	GI:13435809	
VERSION				
KEYWORDS				
SOURCE	Mus musculus			
ORGANISM	Mus musculus (house mouse)			
REFERENCE				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scaplen, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tohiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Zhyvynski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903 (2002)
PUBMED	12477932			
REFERENCE	2	(bases 1 to 2015)		
AUTHORS	Strausberg, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Lohar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.			
FEATURES	source			
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CDS

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ORIGIN

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RESULT 11
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 SOURCE synthetic construct
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 AUTHORS Gao, Z.
 TITLE Murine cytokine receptor
 JOURNAL Patent: WO 0204519-A 6 17-JAN-2002;
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VERSION	AX350978.1	GI:18616354	
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SOURCE	unidentified		
ORGANISM	unclassified sequences.		
REFERENCE	1		
AUTHORS	Gorman, D.M.		
TITLE	Mammalian receptor proteins; related reagents and methods		
JOURNAL	Patent: WO 0190358-A 12 29-NOV-2001;		
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US-10-719-202-2 (1-674) x AX350978 (1-2094)			
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Db	61	YTNARGMGNYYATGTCARCCNCARGAYACGNCMGNTGYWSNYTNGGNTYNSNTGYCAY	120
Qy	41	LeuTrrAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
Db	121	YNTGGGAYGGNGAYGTNTYTNTCCNGGWSNYTNCARWSNCCNCCNGCNGNTN	180
Qy	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
Db	181	YNTGTCNCACNMGNTYTCARACNGARYTNGTYTNGMTGYCCNCARAACNGAYTGY	240
Qy	81	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrrAlaGluProGlu	100
Db	241	GCNYTNTGYTNGMGNTGNTGNTCAYTNGCNGTNCAYGNCNCAYTGGCNGARCCNGAR	300
Qy	101	GluAlaGlySerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln	120
Db	301	GARGCNGGNAARWSNGAYWSNGARYTNCARGARWSNMGNAAYCCNWSNYTNCARGCNCAR	360
Qy	121	ValValLeuSerPheGlnAlaTrrProIleAlaArgCysAlaLeuLeuGluValGlnVal	140
Db	361	GTNGTYTWSNTTYCARGCNTAYCCNATHGCMGNTGYGCNTYNTNGARGTNCARGTIN	420
Qy	141	ProAlaAspLeuValGlnProGlyGlnSerValClySerAlaValPheAspCysPheGlu	160
Db	421	CCNGCNGAYTNGTNCARCCNGGNCARWSNGTNGGWSNCCGNTTYTGATGTYTGAR	480
Qy	161	AlaSerLeuGlyAlaGluValGlnIleTrrSerTrrThrLysProArgTrrGlnLysGlu	180

Db	481	GCWSNYTNGCNGARGTNCARATHGTGWSNTAYACNAARCCNMGNTAYCARAARGAR	540
Qy	181	LeuAsnLeuThrGlnGlnLeuPro-----	188
Db	541	YTNAAYTNCACNCARCAHYTNCNCNGAYTYMGNGGNTNGARGTNGMGNGAYWSNATHCAR	600
Qy	189	-----AspGlyAspAsnValLeuLeuThr	196
Db	601	WSNTGYTGGTYTNCNTGGYTNAAYGTWWSNACNGAYGGNGAYAAAYTNTYNTNACN	660
Qy	197	LeuAspValSerGluGluGlnAspPheSerPheLeuLeuTrrLeuArgProValProAsp	216
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Qy	217	AlaLeuLysSerLeuTrrTrrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHis	236
Db	721	GCNTYNAARWSNYTNTGTYAARAAAYTTCNCGNCCNCARAAYATHACNTYNTAAAYCAY	780
Qy	237	ThrAspLeuValProCysLeuCysIleGlnValTrrSerLeuGluProAspSerGluArg	256
Db	781	ACNGAYTNGTNCNTGYTNTGYATHCARGTNTGGWSNYTNGARCCNGAYWSNGARGMN	840
Qy	257	ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrrHisIleAla	276
Db	841	GTNGARTTYTGYCCNTTYVMNGARGAYCCNGGNCNCAYMGNAAYTNTTGGCAYATHGCN	900
Qy	277	ArgLeuArgValLeuSerProGlyValTrrGlnLeuAspAlaProCysCysLeuProGly	296
Db	901	MGNTYTMGNTYTNWSNCCNGGNTGTGGCARYTNGAYGCNCNTGYTYTTCNCGN	960
Qy	297	LysValThrLeuCysTrrGlnAlaProAspGlnSerProCysGlnProLeuValProPro	316
Db	961	AARGTACNTYNTGYTGGCARGCNCNGAYCARWSNCCNTGYCARCCNYTNGTNCNCN	1020
Qy	317	ValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHis	336
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Qy	337	ProAsnLeuCysValGlnValSerThrTrrGluLysValGlnLeuGlnAlaCysSerTrr	356
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Qy	357	AlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMetLysThrGlyLeu	376
Db	1141	GCNGAYWSNYTNGCNCNTTYAARGAYGAYATGYTNTYNTGNTGARATGAARACNGGNTN	1200
Qy	377	AsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrProLeuProSerMetAla	396
Db	1201	AAAYAYACNWSNGTNTGYCNYTNGARCCNWSNGNTGYACNCCNYTNCNWSNATGGCN	1260
Qy	397	SerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArgSerHisGlnCys	416
Db	1261	WSNACNMGNCNCGNMGNTYNGNGARGARYTNTYNTCARGAYTTCYMGWSNCAAYCARTGY	1320
Qy	417	MetGlnLeuTrrAsnAspAspAsnMetGlySerLeuTrrAlaCysProMetAspLysTrr	436
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Qy	437	IleHisArgArgTrrValLeuValTrrLeuAlaCysLeuLeuLeuAlaAlaLeuPhe	456
Db	1381	ATHCATYMGMTGGGTNTGNTGTYTNGCNYTNTYNTYNTGNCNGCNCNYTNTTY	1440
Qy	457	PhePheLeuLeuLysLysAspArgArgLysAlaAlaArgGlySerArgThrAlaLeu	476
Db	1441	TTTTTYTNTYNTNARAARGAYMGNMGAARCCNCGNMGNGWSNMGNACNGCNYTN	1500
Qy	477	LeuLeuHisSerAlaAspGlyAlaGlyTrrGluArgLeuValGlyAlaLeuAlaSerAla	496
Db	1501	YTNNTCAYSNGCNGAYGGCNGGNTAYGARMGNTYNTGTCGNCNTYNTGNCNWSNCGN	1560
Qy	497	LeuSerGlnMetProLeuArgValAlaValAspLeuTrrSerArgArgGluLeuSerAla	516
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DB	1114	GACCCCTGCCACGCACCTGGTCCCACCGTTTCTCGGAGAACGTCACCTGTGCACAAGGTT	1173
QY	328	GlnAspHeGlnLeuValAlaGlyHisProLenLeuCysValGlnValSerThrTrpGlu	347
DB	1174	CTCGAGTTCCCATTTGCTGAAGGCCACACTTAACCTCTGTGTTCAGGTCAACGATCGG	1233
QY	348	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyPropHelyeAspMet	367
DB	1234	AAGCTGTGACGTCAAGAGTGTGTGGCTGACTCCCTGGGGCCCTCTCAAACGATGTG	1293
QY	368	LeuValGluMetLysThrGlyLeuAenAenThrSerValCysAlaLeuGluProSer	387
DB	1294	CTACTGTTGGACACAGAGCCCCCAGGACAAAGATCCCTCTGTGCTTGGAACCCAGT	1353
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DB	1354	GGCTGTACTTACTATCCACAGAAGCTTCAAGAGGCGAGCTCGCTTGGAGAGTACTTA	1413
QY	408	LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAenAspAsnMetGlySer	427
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QY	428	LeuTrpAlaCysProMetApLyTyrlleHisAargArgTrpValLeuValTrpLeuAla	447
DB	1471	CTATGGGCCCTGCCCATGAGCAATAATCATCCAAAGCGCTGGGCCCTCGTGTGGCTGGCC	1530
QY	448	CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgGlyS	467
DB	1531	TGCTACTCTTTGGCGCTGGCTTTCCTCATCTCTCTCAAAAAGATACGCGAAA	1590
QY	468	AlaAlaArgGlySerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGlu	487
DB	1591	CGCGCCCGCAGGGCGCGCGGCTGTCTCTTACTCAGCCGATGACTCGGTTTCGAG	1650
QY	488	ArgLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValAlaValasp	507
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QY	508	LeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArg	527
DB	1711	CTGTGGAGCCGTCGTGAATGAGCGCGCAGGGGCCGTTGGTTTTCGCGCAGCGGG	1770
QY	528	ArgArglleLeuGlnGluGlyValVallleLeuLeuPheSerProAlaAlaValala	547
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DB	1831	CTGTGACGAGTGGCTCAGAGTGGGTGTCCGGGCCCGGGCGCGACGCGCCGACGAC	1890
QY	565	AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly	584
DB	1891	GCCTTCGCGCCTCGCTCAGCTGCTGTGTGCTGCCGACTTCTTGAGGGCGCGGCGCCG	1950
QY	585	ArgTyrValGlyValTrpPheAspGlyLeuLeuHisProAspSerValProSerProPhe	604
DB	1951	AGCTACGTGGGGCCCTGCTTCGACAGGCTGTCCACCCCGGACGCGCTTTC	2010
QY	605	ArgValAlaProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGln	624
DB	2011	CGCACCGTGCCTCTTACACTGCCCTCCCACTGCCAGACTTCTTGGGGGCCCTGCAG	2070
QY	625	GlyGlyCysSerThrSerAlaGlyArgProAlaAspArgValGluArgValThrGlnAla	644
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 VERSION AX073993.1 GI:12710225
 KEYWORDS Homo sapiens (human)
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Presnell,S.R., Burkhead,S.K. and Powder,S.L.
 TITLE Human cytokine receptor
 JOURNAL Patent: WO 0104304-A 1 18-JAN-2001;
 ZymoGenetics, Inc. (US)
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ORIGIN

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Percent Similarity:	67.4%	Mismatch:	136
Best Local Similarity:	65.3%	Indels:	19
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Ds:			

US-10-719-202-2 (1-674) x AX073993 (1-2255)

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Qy	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
Db	214	CTGGAGAGGCTTGTGGGGCCCTCAGAGCGCTACCACCTGCTCTCCGGGCTCTCTCTCCGC	273
Qy	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
Db	274	CTCTGGGACAGTGACATACTCTGCTGCTGGGACATCGTGCTGCTGCTCGGGCCCGGTG	333
Qy	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnIysThrAspCys	80
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Qy	81	AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100

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Qy 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaAArgCysAlaLeuLeu 136
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Qy 177 TyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro----- 188
Db 694 TACGAGAAGGAACCAACACACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
Qy 189 ---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe 207
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VERSION CS255725.1 GI:86476548
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ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: EP 1621620-A 161 01-FEB-2006;
Genetech, Inc. (US)
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US-10-719-202-2 (1-674) x CS255725 (1-2380)

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DB	653	GAGGTGCAAGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	712
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DB	713	GACTGCTCGAGGCTGGCTTGGAGTGGAGTACGAATCTGGTCTTACTACTGAGCCAGG	772
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DB	893	TCCTCTGTATGGAACTCAGGTTCAGGGCCCCCAAAACCCCGGTGGCAAAAACCTGACT	952
QY	228	GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal	247
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1253	CTCGAGTTCCCAITGGCTTAAAGGCCACCCCTTAACTCTGTGTTCAGGTGAACAGCTCGGAG	1312	Db
348	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet	367	QY
1313	AAGCTGCAGCTGCGAGGAGTGTGTGGCTGACTCCCTCGGGGCTCTCAAAGACGATGTG	1372	Db
368	LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer	387	QY
1373	CTACTGTGGAGACACGAGGCCCCCGACGACACACAGATCCCTCTGTGCTTGGAAACCCAGT	1432	Db
398	GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu	407	QY
1433	GGCTGTACTCTACATACCCAGCAAGACCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTA	1492	Db
408	LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySer	427	QY
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428	LeuTrpAlaCysProMetAspLysTyriLeHisArgArgTrpValLeuValTrpLeuAla	447	QY
1550	CTATGGGCTGCCCCATGGACAATACATACCAAGCGCTGGGCCCTCGTGTGCTGGCC	1609	Db
448	CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys	467	QY
1610	TGCTACTCTTTTGGCGCTGGCTTTCCCTCATCTCTCTCTCAAAGAGATCAAGCGGAA	1669	Db
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474	ThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyriGluArgLeuValGlyAlaLeu	493	QY
1727	CGGGCTGTGCTCTCTACTCAGCCGATGACTCGGGTTTCGAGCGCTGTGTGGCGCCCTG	1786	Db
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534	GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu	553	QY
1907	GGCGGCTGGTGGTCTTGCTCTCTCCGGTGGCGTGGCGCTGTGACGAGCGAGTGCCTA	1966	Db
554	GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu	570	QY
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 09:00:24 ; Search time 339 Seconds
(without alignments)

5580.209 Million cell updates/sec

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Perfect score: 3605

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Database :

Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2281	63.3	2622	3	US-10-104-047-1326
3	316.5	8.8	2138	3	US-09-747-259-15
4	310.5	8.6	2165	3	US-09-188-930-226
5	310.5	8.6	2165	3	US-09-312-283C-226
6	193.5	5.4	681	3	US-09-893-737-327
7	174.5	4.8	3288	2	US-08-620-694A-1
8	174.5	4.8	3288	3	US-09-022-255-1

9	174.5	4.8	3288	3	US-09-022-696-1	Sequence 1, Appli
10	174.5	4.8	3288	3	US-08-978-773-1	Sequence 1, Appli
11	174.5	4.8	3288	3	US-09-022-253-1	Sequence 1, Appli
12	174.5	4.8	3288	3	US-09-022-260-1	Sequence 1, Appli
13	174.5	4.8	3288	3	US-09-022-259-1	Sequence 1, Appli
14	174.5	4.8	3288	3	US-09-022-257-1	Sequence 1, Appli
15	174.5	4.8	3288	3	US-09-549-679-1	Sequence 1, Appli
16	174.5	4.8	3288	5	US-09-488-728-1	Sequence 1, Appli
17	154	4.3	3120	2	US-09-949-002-117	Sequence 117, App
18	154	4.3	3223	2	US-08-620-694A-9	Sequence 9, Appli
19	154	4.3	3223	3	US-09-022-255-9	Sequence 9, Appli
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26	154	4.3	3223	3	US-09-549-679-9	Sequence 9, Appli
27	154	4.3	3223	5	US-09-488-728-3	Sequence 3, Appli
28	152	4.2	3120	3	US-09-949-002-126	Sequence 126, App
29	149	4.1	1059	3	US-09-188-930-6	Sequence 6, Appli
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31	146	4.0	7291	3	US-09-949-016-12425	Sequence 12425, A
32	146	4.0	7299	3	US-09-949-016-15948	Sequence 15948, A
33	138	3.8	28976	3	US-09-949-002-689	Sequence 689, App
34	138	3.8	28976	3	US-09-949-002-698	Sequence 698, App
35	137.5	3.8	3105	3	US-09-252-991A-12350	Sequence 12350, A
36	137.5	3.8	26104	3	US-09-949-016-14045	Sequence 14045, A
37	137.5	3.8	77626	3	US-09-949-016-12608	Sequence 12608, A
38	136.5	3.8	4022	3	US-10-104-047-293	Sequence 293, App
39	136	3.8	44430	3	US-09-949-016-12468	Sequence 12468, A
40	136	3.8	44431	3	US-09-949-016-15882	Sequence 15882, A
41	134	3.7	8367	2	US-08-583-562B-7	Sequence 7, Appli
42	134	3.7	8367	2	US-08-779-113-7	Sequence 7, Appli
43	134	3.7	8368	3	US-09-949-016-211	Sequence 211, App
44	134	3.7	8368	3	US-09-949-016-4986	Sequence 4986, App
45	132	3.7	40325	3	US-09-949-002-580	Sequence 580, App

ALIGNMENTS

RESULT 1

US-09-747-259-13
; Sequence 13, Application US/09747259

; Patent No. 6569645

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

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; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1 (US)

; CURRENT APPLICATION NUMBER: US/09/747,259

; CURRENT FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

Qy	302	TrpGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGlnIlyAsn	321	Qy	645	LeuArgSerAlaLeuAspSerCys-----ThrSerSerSerGluAlaProGly	660
Db	1420	TGGCGGCTCCGGTGGGGACCCCTGTCAGACCACTGGTCCCAACCGCTTCCTCCGGGAGAAAT	1479	Db	2494	CTTCAGCCGACCTCGATAGCTACTTCCATCCCGGGGACTCCCGCGCGGGA	2547
Qy	322	AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysVal	341	Qy	322	AlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysVal	341
Db	1480	GTCACCTGTGACAAAGGTTCTCGAGTTCCTCCATTCCTGAAGGCCACCTTAACCTCTGTGT	1539	Db	1480	GTCACCTGTGACAAAGGTTCTCGAGTTCCTCCATTCCTGAAGGCCACCTTAACCTCTGTGT	1539
Qy	342	GlnValSerThrTrpGluIlyValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGly	361	Qy	342	GlnValSerThrTrpGluIlyValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGly	361
Db	1540	CAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGAGAGTGTGTGTGGCTGACTCCCTCGGG	1599	Db	1540	CAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGAGAGTGTGTGTGGCTGACTCCCTCGGG	1599
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Db	1600	CCTCTCAAGACGATGTGCTACTGTGGAGACAGAGGCCCCAGACACAGATCCCTC	1659	Db	1600	CCTCTCAAGACGATGTGCTACTGTGGAGACAGAGGCCCCAGACACAGATCCCTC	1659
Qy	382	CysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla	401	Qy	382	CysAlaLeuGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAla	401
Db	1660	TGTGCTTGAACCCAGTGGCTGTACTTCACTACCCAGCAAGCTCCAGAGGGCAGCT	1719	Db	1660	TGTGCTTGAACCCAGTGGCTGTACTTCACTACCCAGCAAGCTCCAGAGGGCAGCT	1719
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Db	1777	GACGATGACTTGGGAGCGCTATGGCGCTGCCCATGACAAATACATCCACAAGCGCTGG	1836	Db	1777	GACGATGACTTGGGAGCGCTATGGCGCTGCCCATGACAAATACATCCACAAGCGCTGG	1836
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Db	2134	CGCCAGACCTCGAGAGGGCGGTGGTGGTGTGTCTCTCTCCGGTGGCGGTGGCG	2193	Db	2134	CGCCAGACCTCGAGAGGGCGGTGGTGGTGTGTCTCTCTCCGGTGGCGGTGGCG	2193
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Qy	565	AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly	584	Qy	565	AlaLeuAlaAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGly	584
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Db	2314	AGTACTGTGGGGCGCTGTCTGACAGGCTGTCTCCACCGGAGCGGTACCCGCTTTC	2373	Db	2314	AGTACTGTGGGGCGCTGTCTGACAGGCTGTCTCCACCGGAGCGGTACCCGCTTTC	2373
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Qy	33	sSerLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuProGlySerLe	53
Db	467	CTCAGA-GGAAGCTGCTGCTCGTC-----GTCCCTGTCTGAGAGAGCCAT	513
Qy	53	uGlnSerAlaProGlyProValLeuValProThrArgLeuGlnThrGluLeuValLeuAr	73
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Db	604	CCAGATTGGACT-----CACAAAGGATGAGAGCC-GAG-----	639
Qy	113	gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTrpProIleAlaArgCy	133
Db	640	-----TTCTCTTTGATTGCTGCTGAGGCCCGCGGC	671
Qy	133	sAlaLeuLeuGluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlyse	153
Db	672	TATTGGGTGACCATA-----	687
Qy	153	rAlaValPheAspCysPheGluAlaSerLeuGlyAlaGluValGlnIle-----	169
Db	688	-----TCTTCAGGCCCTGAGGTTCAGCGTCTTTGTCA	722
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Qy	208	uLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThrGl	228
Db	772	-----AAAAATTGTGTGG	785
Qy	228	yProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnValTr	248
Db	786	GGGCCACACTGTAGAGCTGCTTATGAATTCTTCTGCCCTGTCTGTGCATAGAGGCATC	845
Qy	248	pSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAl	268
Db	846	CTACCTGTCAAGAGGACACTGTGAGGGCGCAAAATGTCCCTTCCAGAGCTGGCCAGAGC	905
Qy	268	aHis---ArgAsnLeuTrp-----HisIleAlaArgLeuArgValLeuSerProGl	284
Db	906	CTATGGCTCGGACTTCTGGAAGTCAGTGCACCTTCACCTGACTACAGCCAGCAGCAT	965
Qy	284	yValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAl	304
Db	966	GGTCATGGCCCTGACACTCGCTGCCCACTGAAGCTGAAGCTGCCCTCTGCCAGAGGCA	1025
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Qy	341	lGlnValSerThrTrpGluLysValGlnLeuGlnAlaCys-----SerTr	356
Db	1128	-CAAGTTCTCTTTTGGAAACAG-----CAGCCATGTTGAATGCCCCAGCAGACTG	1177
Qy	356	pAlaAspSerLeu-----GlyProPheLysAspAspMetLe	368
Db	1178	GGTCTCTCATCTCTGGAAATGTAAAGCATGGATATCCCAAGCCCAAGAGCTATTTCTTCACT	1237
Qy	368	uLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-SerG	388
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Qy	388	lyCys-----ThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyG	405
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Db	1406	GGCGGTGAGAT---GTCCAGTTTGGCTTGAAGCAGCCTTCTGTGTCCAGATGTCTTTACA	1462
Qy	437	leHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuLeuAlaAlaLeuPheP	457
Db	1463	GACACTGGGG-----CTCTTGATCTTGGCACTGTCTGCCCTCTCACCTACTGGGTG	1516
Qy	457	hePheLeuLeuLysLysAspArgLysAlaAlaArgGly---SerArgThrAlaL	476
Db	1517	TTGTTCTGGCCCTCACCTGCGGCGCCACAGTCAGGCGCCCGGCGGCGGCGGCTGCG	1576
Qy	476	euleLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerA	496
Db	1577	TCCTCTGCAAGCGGCGGAGCTCGAGGGCGAGCGGCGGCTTGTGGAGAGCGCTGGCTGAAC	1636
Qy	496	laLeuSerGlnMet-----ProLeuArgValAlaValAspLeuTrpSerArgArg	513
Db	1637	TGCTACGCGCAGCGCTGGGCGGCGGCGGAGCTGATCTGTGGACCTGTGGAGGGAGGC	1696
Qy	513	luLeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleuGlnG	533
Db	1697	ACGTGCGCGCGTGGGCGCGCTGCGCGTGGCTCTGGGCGGCGCGGCGCGCTAGCGCGG	1756
Qy	533	luGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpL	553
Db	1757	AGCAGGGCAGCTGT	1791
Qy	553	euglnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysV	573
Db	1792	--GACCTTGGCGCGTACAG---GGCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCG	1842
Qy	573	aLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspG	593
Db	1843	-----CTGCTCCAGCTGCGCGCGCGCGCGCTGCTGTCTGTCTTACTTCACTC	1891
Qy	593	lyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuP	613
Db	1892	GCCTCTGCGCCCAAGGGCGACATCCCGCGCGCGCTGCGCGCGCTGCGCGCTACCGCCTGC	1951
Qy	613	roThrGlnLeuProAlaPheLeuAspAlaLeuGlnGly-----GlyCysSerThrS	630
Db	1952	TGGCGGACTGCGCGCTGTCTGCGGGGCTGTGAGCGCGCGGCTTTCGAGAGGCCACCA	2011
Qy	630	eAlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuA	650
Db	2012	GCTGGGGCGCTTGGGGCGGCGGCGAGCGAGG-----CAGAGCGCGCTAG	2056
Qy	650	spSerCysThr-----Sers	655
Db	2057	AGCTGTGCGAGCGCGCTTGAACGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2116

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```

QY 655 erSerGluAlaProGlyCys 661
Db 2117 TCACCCGAGTCCGGGTGT 2136

RESULT 4
US-09-188-930-226
; Sequence 226, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-226

Alignment Scores:
Pred. No.: 2,22e-20 Length: 2165
Score: 310.50 Matches: 129
Percent Similarity: 37.5% Conservative: 52
Best Local Similarity: 26.7% Mismatches: 101
Query Match: 8.6% Indels: 18
DB: 3 Gaps: 18

US-10-719-202-2 (1-674) x US-09-188-930-226 (1-2165)
QY 224 LysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeu 243
Db 616 AAATTGTGTGGGCCACACTGTAGACCTGCTTATGAAATTCCTTCTGCTCCGTCGATG 675
QY 244 CysIleGlnValTrpSerLeuGluProAspSerGluArgValGluPheCysProPheArg 263
Db 676 TGCATAGAGGCTCTACCTGCAAGAGGACACTGTGAGGCGCAAAAGTGTCCCTCCAG 735
QY 264 GluAspProGlyAlaHis---ArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSer 282
Db 736 AGCTGGCTGAGCTTATGGCTCAGACTTCTGGCAGTCAATACGCTTCACTGACTACAGC 795
QY 283 ProGly-----ValTrpGlnLeuAspAlaProCysCysLeuProGlyLysValThr 299
Db 796 CAGCACAATCAGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
QY 300 LeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeuValProProValProGln 319
Db 856 CTCTGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 897
QY 320 LysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGly-----His 336
Db 898 CCCAACGCCACAGCAGAGGAGTCAAGAGGATGATGATGATGATGATGATGATGATGATGAT 957
QY 337 ProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGlnAlaCys----- 354
Db 958 CCCACAGCTCTGCTTTAAGTTCTCA---TTTGAACACAGCAGCAGCAGTGTGATGCTCCAC 1014
QY 355 -----SerTrpAla-----AspSerLeuGlyProPheLysAsp 365
Db 1015 CAGAGTGGCTCTCTCCATCTCTGGACTGTGAGCATGGATAGCACA-GGCCAGCAGCTGAC 1073
QY 366 AspMetLeuValGluMetLysThrGlyLeuAsnThrSerValCysAlaLeuGlu 385
Db 1074 GCTTCACTTTCTTCGAGGACATATGCCCACCTTCAG-----TGCTGCTGGAG 1121

386 -ProSerGlyCys-----ThrProLeuProSerMetAlaSerThrArgAlaAlaAr 402
1122 TGACCCAGGTTTGGGGCGGATACCCCTCTGTGTACAGCATCAGCCAGACCCA 1181
QY 402 gLeuGlyGluGluLeuGlnAsp-----PheArgSerHisGlnCysMe 417
1182 GGGCTCAGTCCAGTCAGCGTAGACCTCATCCCTTCTCTGAGGAGGAGGAGGAGGAGGAGG 1241
QY 417 tGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaCysProMetAspLysTrpI 437
1242 CTTGGTGGAGTCCAGAT-----CGTCCCTTAGGCTCCGG 1262
QY 437 eHisArgArgTrpValLeuVal-----TrpLeuAlaCysLeuLe 450
1263 CCATTTTGGCTGGAAGCAGCTTTGTGTCTGTATGATGCGCCCTTACCTTACTCAGCTGT 1322
QY 450 uLeuAlaAlaAlaLeuPhePheLeuLeuLeuLysAspArgArgLysAlaAlaAr 470
1323 GCTC-----CGTCCCTTAGGCTCCGG 1343
QY 470 gGlySerArgTrpAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLeuVa 490
1344 TCGAACAGGCGCAGTTTACTCTTACTATGACGGAGCTCAGAGGACACGACGCGCTGTGT 1403
QY 490 lGlyAlaLeuAlaSerAlaLeuSerGlnMet-----ProLeuArgValAlaValAs 507
1404 GGGAGCTTTGGCCGAACCTGCTGGGAGCGGCTGGGAGGTGGAGCGACGCTATCGTGA 1463
QY 507 pLeuTrpSerArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnAr 527
1464 TCTCTGGGAAGGACGACGATGACGATGACGATGACGATGACGATGACGATGACGATGACG 1523
QY 527 gArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSerProAlaAlaValAl 547
1524 GAGCGCGTGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1583
QY 547 aGlnCysGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAl 567
1584 C-----ACCGCTGCGAGCGGTGACCCGCGAGCGGTGCTCCCT 1619
QY 567 aAlaTrpLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpVa 587
1620 TCGACACCTTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1655
QY 587 lGlyValTrpPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAl 607
1656 GCTGCGCTTACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1715
QY 607 aProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCy 627
1716 GCCAGCTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1775
QY 627 sSerThrSerAla-----GlyArgProAlaAspArgValGluArgVa 641
1776 TGCCACCTTACCTTCCAGCTGAGTGCACCTTGGGCTAAGCGGTGCTTGAACCCGCT 1835
QY 641 lThrGlnAla-----LeuArgSerAlaLeuAspSerCysThrSerSerSerGl 657
1836 GGAGCAGTGTCACTGCTGGAACCTTGGAGCTGCCAAGATGACTACCAAGGCTCAACCA 1895
QY 657 uAlaPro 659
Db 1896 TAGTCCC 1902

RESULT 5
US-09-312-283C-226
; Sequence 226, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene

```


us-10-719-202-2.2.p2n.rn1

Tue Aug 22 11:34:35 2006

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; LOCATION: (1)... (681)
US-09-893-737-327

Alignment Scores:      1.43e-09      Length:      681
Pred. No.:            193.50      Matches:      73
Score:                42.2%      Conservative: 21
Percent Similarity:   32.7%      Mismatches:  102
Best Local Similarity: 5.4%      Indels:      27
Query Match:         3          Gaps:        7
DB:

US-10-719-202-2 (1-674) x US-09-893-737-327 (1-681)

QY 438 HisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuAlaAlaLeuPhePhe 457
Db 31 TACAGACACCTGGGGCTCTTATCTGGCATCTGCTGGCCCTCTCCACCTACTGGGTGTT 90
QY 458 PheLeuLeuLeuLysAspArgArgLysAlaAlaArgGly---SerArgThrAlaLeu 476
Db 91 GTTCTGGCCCTCACCTGGCGGCCACAGTCAGCGCGGCCGCCAGCGCGCCAGTGTCTC 150
QY 477 LeuLeuHisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAla 496
Db 151 CTCTGTGACCGCGGCACTCGAGGCGCGAGCGCGCCCTGGTGGAGCCCTGCTGTAAGTG 210
QY 497 LeuSerGlnMet-----ProLeuArgValAlaValAspLeuTrpSerArgArgGlu 513
Db 211 CTACGGGCGAGCGCTGGCGCGCGCGCGCGCGATGATCGTGGACCTGTGGAGGGAGGCAC 270
QY 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgArgIleuGlnGlu 533
Db 271 GTGGCGCGCTGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
QY 534 GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
Db 331 CAGGGGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
QY 554 GlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTrpLeuSerCysVal 573
Db 364 GACCTTGGCCCGGTGACG---GGCCCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCG 414
QY 574 LeuProAspPheLeuGlnGlnArgAlaThrGlyArgTyrValGlyValTyrPheAspGly 593
Db 415 -----CTGTCTCCACGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 465
QY 594 LeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuPro 613
Db 466 CTCTGGCCCAAGGCGGACATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 525
QY 614 ThrGlnLeuProAlaPheLeuAspAlaLeuGlnGly-----GlyCysSerThrSer 630
Db 526 CGCGACCTGCGCGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 585
QY 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
Db 586 TGGGCGCCCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 630
QY 651 SerCysThr 653
Db 631 CTGTGTCAGC 639

RESULT 7
US-08-620-694A-1
; Sequence 1, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fenslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
```


Db 550 TTTTCCTTCAGCCACTTTGGTAGATCCTGGC----- 582
Qy 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGAGATGATGAAGTACTGTT-----CACCACCTG 612
Qy 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCATCCCTGATGGGACCCCAACCAAAATCCA----- 652
Qy 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
Db 653 -----AGATCATCTTTTGGCTGACTGTGAGACACAGAGATGAAGATGACTACCTCA 705
Qy 346 -----TTPGLuLysValGlnLeuG1 352
Db 706 TGGGTGAGCTCAGCAGCCCTTTGGGATCCCAATCATCTGTGGAGACTTGGACACACAG 765
Qy 352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe 372
Db 766 CATTCGGAGTGG----- 778
Qy 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389
Db 779 -----ACTTCACCTGTGGAAATGAATCCACCCCTACCAGGTCTCTG 819
Qy 389 sThrProLeu-----ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLe 408
Db 820 CTGGAAGTTTCTCCGACTCAGACACCACTGCTTGTGATGCTGTTAAACAATATTT 879
Qy 408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspMetGlySerLe 428
Db 880 GCGCCAGCAGCAAGAAGATCCATCAGCGAGCTAATGTGCATTC-ACTTAAGCAAGTT 938
Qy 428 u-----TrpAlaCys----- 431
Db 939 TCACTGTGTGCTGCCATCACCAGTGCAGTCCAGCCCTTCTTCAGCAGCTGCCCTAAATGA 998
Qy 431 ----- 431
Db 999 CTGTTTGAGACACGCTGTGATGTCGCCCTGCCAGTAATCTCAAAATACCACAGTTCCAA 1058
Qy 432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
Db 1059 GCCAGTTGCAGACTACATT---CCCTGTGGGTGATGAGCTCATCATCTCATCGCCAT 1115
Qy 449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
Db 1116 TCTGCTGTGGATCTGTCATCGTGTGATCATCTGTATGACCTGGAGGCTTTCTGGCGC 1175
Qy 463 sAspArgArgLysAlaAlaArgGlySer----- 472
Db 1176 CGATCAAGAGAAACATGGTGATGATCTCAAAATCAATGAGCATCTTGGCCGTAGCAGACCT 1235
Qy 473 -----ArgThrAlaLeuLeuHisSerAlaAspGlyAlaGl 485
Db 1236 GACTCCCCCACCCTGAGGCCAGAGGTGTGATCTGTACTGCGCCGACACCCCT 1295
Qy 485 YTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu-----SerGlnMetProLeuArgVa 504
Db 1296 CTATGTGGAGTGGTCTCTAAAGTTCCGCCATTCCTGATCCTGCTGCTGCTGCTGCTGCTGCT 1355
Qy 504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
Db 1356 AGCCCTTGACTCTCTGAGAGCAGAGGTATCTCTGAGGTGGGGTCAATGACCTGGGTGAG 1415
Qy 524 sHisGlnArgArgIleLeuGlnGluGlyValValValIleLeuLeuPheSer----- 542
Db 1416 CCGACAGAGCAGAGATGTTGGAGACCACTCCAAATCATCTCTGTGTCTCCGAGG 1475
Qy 543 -----ProAlaAlaValAlaGlnCy 549
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Db 1476 CACCCAGCAAAAGTGAAGAGCTATCTTGGTTGGCTGAGCCCTGCTGTCTCAGCTACGGTG 1535
Qy 549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaAlaTr 569
Db 1536 TGACCACTGG-----AAGCCTGCT---GGGACCTTTTCACTGCGAGC 1574
Qy 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
Db 1575 CATGAACATGATCTCTCCAGACTTCAAGAGGCCAGCTGCTTGGCAGCTACGTTGTTTG 1634
Qy 589 lTyTrpPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
Db 1635 CTACTTCAGTGGCATCTGTAGTGAGAGGATGTCCTCCGACCTCTTCAACATCACCTCCAG 1694
Qy 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
Db 1695 GTACCCACTCATGACAGATTTGAGGAGGTTTACTTCCGGATCCAGGACCTGGAGATGTT 1754
Qy 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
Db 1755 TGAACCCGCGCGATGTCACCATGTCTCAGAGAGCTCACAGGGGACAAATTACCTGCGAGGCC 1814
Qy 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerGluAlaP 659
Db 1815 TAGTGCCCGCAGCTCAAGAGGCTGTGCTTAGGTTCCAGGAGTGCGCAAAACCCAGTGCCC 1874
Qy 659 ro 659
Db 1875 CG 1876
RESULT 8
US-09-022-255-1
; Sequence 1, Application US/0902255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: HVS13 receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2715
US-09-022-255-1

Alignment Scores:
Pred. No.: 1.5e-06 Length: 3288
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
Best Local Similarity: 20.4% Mismatches: 192
Query Match: 4.8% Indels: 207
DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-09-022-255-1 (1-3288)

QY 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
DB 316 AAAACCTGACCCCGCTCTCCCAAAACATCTATATCAATCTTAGTGTTCCTCTTACC 375
QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
DB 376 CAGCAGGAGAAATAGTCCCTGTGTTCATGTGAG---TGGACCTCGACAGATGCC 432
QY 254 -----SerGluArg 256
DB 433 AGCATCCTGTACTCAGAGGTGAGAGTGTCCGTCTGACGTGAACACCAATGAGCGG 492
QY 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
DB 493 CTGTGTGTCAGTTC---CAGTTTCTGCTCCATGCTGCAGCATCACCGTAAAGCGGTGGCGG 549
QY 275 IleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
DB 550 TTTTCTCTTCAGCCACTTGTGGTAGATCCCTGGC----- 582
QY 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
DB 583 CAGGAGTATGAAGTACTGTT-----CACCCACCTG 612
QY 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
DB 613 CCGAAGCCCATCCCTGTAGTGGGACCCCAACACCAATCCA----- 652
QY 333 LAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
DB 653 -----AGATCATCTTTGTGCTGCTGTGTGAGCAGCAGCAAGATGAAGATGACTACTCA 705
QY 346 -----TrpGluLysValGlnLeuG1 352
DB 706 TGCCTGAGCTCAGCAGCCTTTGGGATCCCAACATCATCTGTGGAGACCTTGGACACACAG 765
QY 352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe 372
DB 766 CATCTGCCAGTGG----- 778
QY 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCys 389
DB 779 -----ACTTCACCTGTGGGAATGAATCCACCCCTACCGAGTCTG 819
QY 389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLe 408
DB 820 CTGGAAGTCTTCGCACTCAGAGNACCAGCAGTGTCTTGTGTCGTTTAAACAATATTT 879

QY 408 uGlnAspPheArgSerHisGlnCysMetClnLeuTrpAsnAspAspAsnMetGlySerLe 428
DB 880 GGGCCAGGCAAGAAGATTCATCAGCGAGCTAATGTTCATTC-ACTTAAGCAAGTT 938
QY 428 u---TrpAlaCys----- 431
DB 939 TCACGTGCTGCCATCACCACGTGCAGGCTTCCTTCAGCAGCTGCCTAATGA 998
QY 431 ----- 431
DB 999 CTGTTTGAGACACGCTGTGACTGTGCCCTGCCAGTAATCTCAATAACACAGATTCCTCA 1058
QY 432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
DB 1059 GCCAGTTGCAGACTCATTT---CCCCGTGGGTGTATGGCTTCATCACATCATCGCCAT 1115
QY 449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLeu 463
DB 1116 TCTGCTGGTGGATCTGTATCGTGTGATCATCTGTATGACCTGGAGGCTTTCTGGCGC 1175
QY 463 sAspArgArgLysAlaAlaArgGlySer----- 472
DB 1176 CGATCAAGAGAAACATGCTGATGACTCCAAAATCAATGGCATCTTGCCCGTAGCAGACCT 1235
QY 473 -----ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaG1 485
DB 1236 GACTCCCCCACCCTGAGGCGCCAGGAAGTCTGGATCTGTACTTCGCCGCCACCCCT 1295
QY 485 yTyrgluArgLeuValGlyAlaLeuAlaSerAlaLeu---SerGlnMetProLeuArgVa 504
DB 1296 CTATGTGGAGTGGTCTCTAAAGTTGCGCCAGTCTCTGATCATCTGCTGTGGCACTGAAGT 1355
QY 504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
DB 1356 AGCCCTTGACCTCTGGAGAGCAGGTTATCTCTGAGTGGGGTCTGATGCTGGTGAG 1415
QY 524 sHiseLnaArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSer----- 542
DB 1416 CCGACAGAAGCAGGAGATGGTGGAGAGCACTCCAAAATCATCATCTGTGTTCGGAGG 1475
QY 543 -----ProAlaAlaValAlaGlnCys 549
DB 1476 CACCAAGCAAGTGAAGACTATCTTGGGTGGGCTGAGCCTGTCTCCAGTACGCTG 1535
QY 549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
DB 1536 TGACCACTGG-----AAGCCTGCT---GGGGACCTTTTCACCTGCAGC 1574
QY 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
DB 1575 CATGAACATGATCTCTGCCAGACTTCAGAGGCCAGCCTGCTTCGGCACCTACGTTGTTG 1634
QY 589 lTyrrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProle 609
DB 1635 CTACTTCAGTGGCATCTGTAGTGAAGGGATGTCCCGACCTCTTCAACATCATCCTCCAG 1694
QY 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
DB 1695 GTACCCACTCATGGACAGATTTGAGAGGTTTACTTCGGATCCAGGACCTGGAGATGTT 1754
QY 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
DB 1755 TGAACCCCGCCGATGTCACCATGTCCAGAGAGCTCACAGGGGCAATTTACTTCGACAGCCC 1814
QY 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAla 659
DB 1815 TAGTGGCCGCGCAGCTCAAGGAGGCTGTGTTAGGTTCCAGGAGTGGCAAAACCAGTGCCC 1874
QY 659 ro 659
DB 1875 CG 1876
RESULT 9

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Mouse
 IMMEDIATE SOURCE:
 CLONE: IL-17 receptor
 NAME/KEY: CDS
 LOCATION: 121..2712
 US-08-978-773-1

Alignment Scores:
 Pred. No.: 1,5e-06 Length: 3288
 Score: 174.50 Matches: 119
 Percent Similarity: 31.6% Conservative: 65
 Best Local Similarity: 20.4% Mismatches: 192
 Query Match: 4.8% Indels: 207
 DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-08-978-773-1 (1-3288)

QY	224	LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn-----	235
DB	316	AAAAACCTGACCCCGCTTCCCAAAAAACATCTATATCATCTTAGTGTTCCTCTACC	375
QY	236	---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp---	253
DB	376	CAGCAGCGAGAAATTAGTCCTGTGTTCATGTTGAG---TGGACCTCGCAGACAGATGCC	432
QY	254	-----SerGluArg 256	
DB	433	AGCATCTCTGACCTCGAGGGTGCAGAGTGTCCGCTCCTGAGCTGAACCAATGAGCGG	492
QY	257	-----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis	274
DB	493	CTGTGTCTCAAGTTC---CAGTTCCTGTCATGCTGCAGCATCACCGTAAGCGGTGGCGG	549
QY	275	IleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys	293
DB	550	TTTTCTTCAGCCACTTTTGGGTAGATCTCTGGC-----	582
QY	294	LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu	313
DB	583	CAGGAGTATGAGTGACTGTT-----CACACCTGT 612	
QY	314	ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa	333
DB	613	CCGAAGCCCATCTCTGATGGGACCCCAACCAATCCA-----	652
QY	333	LAlaGlyHisProAsnLeuCysValGlnValSerThr-----	345
DB	653	-----AGATCATCTTTGTGCTGACTGTGTGAGGACAGCAAGATGAAGATGACTACTCA	705
QY	346	-----TrpGluLysValGlnLeuG1 352	
DB	706	TGCGTGAGCTCAGCGAGCTTTTGGGATCCCAACATCACTGTGGAGACCTTGGACACAG	765
QY	352	nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe	372
DB	766	CATCTGCGAGTGG-----	778
QY	372	tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCys	389

504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
 1356 AGCCCTGACCTCTCGAAGACAGGATTTATCTCTGAGGTGGGGTGCATGACCTGGGTGAG 1415
 524 sHisGlnArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSer----- 542
 1416 CCGACAGACGAGGATGGTGGAGAGCAACTCCAAATCATCTCTGTGTCTCCGAGG 1475
 543 -----ProAlaAlaValAlaGlnCys 549
 1476 CACCAAGCAAGTGGAAAGCTATCTTGGGTGGGCTGAGCCTGCTGTCAGCTACCGTG 1535
 549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
 1536 TGACCACTGG-----AAGCTGCT---GGGACCTTTTCACTGCAGC 1574
 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
 1575 CATGAACATGATCTGCGCAGACTTCAAGAGCGAGCCTGCTTCGGGACCTAGTGTGTTG 1634
 589 lTyPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
 1635 CTACTTCACTGAGCATCTGTAGTGAGGGATGTCCTCCGACCTTCAACATCACCTCCAG 1694
 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
 1695 GPACCCACTCATGACAGATTTGAGGAGTGTACTTCCGGATCCAGGACCTCGAGATGTT 1754
 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
 1755 TGAACCCGCGGATGACCACTATGTCAGAGAGCTCAGAGGACCAATACCTCGCAGAGCCC 1814
 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlap 659
 1815 TAGTGGCGGCAGCTCAAGGAGGCTGTCTTAGTGTTCAGGAGTGGGAAACCCAGTGCCC 1874
 659 ro 659
 1875 CG 1876

RESULT 10
 US-08-978-773-1
 Sequence 1, Application US/08978773
 Patent No. 6083906
 GENERAL INFORMATION:
 APPLICANT: Trout, Anthony
 TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple PowerMacintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,773
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 60/052,525
 FILING DATE: 27 NOVEMBER 1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2623-A


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US-10-719-202-2 (1-674) x US-09-022-253-1 (1-3288)
QY 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAAARCTGACCCCGTCTTCCCAAAAAACATCTATATCAATCTTAGTGTTCCTCTACC 375
QY 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGGAGAAATAGTCCCTGTGTGATGTTGAG---TGGACCTGCGACAGATGCC 432
QY 254 -----SerGluArg 256
Db 433 AGCATCTGTACCTGAGGGTGCAGAGCTGTCCGTCTGCAGCTGAACCAATAGCGG 492
QY 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAAGTTC---CAGTTTCTGTCCATGTGTCAGCATCACCGTAAGCGGTGGCGG 549
QY 275 IleAlaArgLeuArg---ValIleSerProGlyValTrpGlnLeuAspAlaProCysCys 293
Db 550 TTTTCCTTCAGCCACTTTGTGTGATCTGTGC----- 582
QY 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTAGAAGTCACTGTT-----CACACACTG 612
QY 314 ValProProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCATCCCTGATGGGAGCCCAACCAATCA----- 652
QY 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
Db 653 ---AGATCATCTTGTGCTGCTGCTGCTGAGGACAGCAAGATCAAGATGACTACTCA 705
QY 346 -----TrpGluLysValGlnLeuG1 352
Db 706 TGGCTGAGCTCAGGACGCTTTGGGATCCCAACATCATCTGTGGAGACCTTGACACAG 765
QY 352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuValGluMe 372
Db 766 CATCTGGAGTGG----- 778
QY 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389
Db 779 -----ACTTCACCTGTGGAATGCAATCCACCCCTACCGAGTCCGTG 819
QY 389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLe 408
Db 820 CTGGAAGTTCCTCCGACTCAGAGACCAACAGCTGCTTTGATGCTGTTAAACAAATATT 879
QY 408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLe 428
Db 880 GCGCCAGGCAAGAAGAAATCCATCAGCGAGCTAATGTCAATTC-ACTCTAAGCAAGTT 938
QY 428 u---TrpAlaCys----- 431
Db 939 TCACTGGTGTGCCATCACACGTCGAGGTCAGCCCTTCTTACGAGCTGCCTAAATGA 998
QY 431 ----- 431
Db 999 CTGTTTGACACAGCTGTGAGTGTGCTGCCCTGCCAGTAATCTCAAATACCAAGTCCCAA 1058
QY 432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
Db 1059 GCCAGTTCAGACTACATT---CCCTGTGGGTGATGGCCCTATCATCATCTCGCCAT 1115
QY 449 uLeuLeuAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
Db 1116 TCTGTGTGGGATCTGTGATGCTGCTGATCATCTGATGATGATGATGATGATGATGATG 1175
QY 463 sAspArgArgLysAlaAlaArgGlySer----- 472
Db 1176 CGATCAAGAGAAACATGGTGTGATGACTCCAAAATCAATGCAATCTTGTGGCCGTAGCAGCT 1235

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QY 473 -----ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGl 485
Db 1236 GACTCCCCACCCCTGAGGCCAGGAGTCTGGATCTGTCTACTCGCGGACACCCCT 1295
QY 485 yTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu---SerGlnMetProLeuArgVa 504
Db 1296 CTATGTGGAGGTGGTCTTAAAGTTCGCCAGTTCCTGATCACTGCTGTGGCACTGAAGT 1355
QY 504 lAlaValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAlaTrpPheHi 524
Db 1356 AGCCCTTGACCTCTCTGGAAGACAGGTTATCTCTGAGGTGGGGTCATGACCTGGGTGAG 1415
QY 524 sHisGlnArgArgArgIleLeuGlnGluGlyValValIleLeuLeuPheSer----- 542
Db 1416 CCGACAGAAAGCAGGATGGTGGAGAGCAACTCCAAAATCATCATCTGTGTTCGGAGG 1475
QY 543 -----ProAlaAlaValAlaGlnCy 549
Db 1476 CACCAAGCAAGTGGAAAGCTATCTTGGTGGGCTGAGCCTGCTGTCCAGCTACGGTG 1535
QY 549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
Db 1536 TGACCACTGG-----AAGCCTGCT---GGGACCTTTTCACTGCAGC 1574
QY 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
Db 1575 CATGAACATGATCTGCCAGACTTCAAGAGGCCAGCCTGCTTCGGCACCTTACCTTGTG 1634
QY 589 lTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
Db 1635 CTACTTCAGTGGCATCTGTAGTGAGAGGGATGTCCCGACCTCTTCAACATCACCTCCAG 1694
QY 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
Db 1695 GTACCCACTATGACAGAGATTGAGGAGGTTTACTCCGGATCCAGGACCTGGAGATGT 1754
QY 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
Db 1755 TGAACCCGGCGGATGCACCATGTGACAGAGCTCACAGGGGACAAATTACTGTGACAGGCC 1814
QY 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlap 659
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QY 659 ro 659
Db 1875 CG 1876

RESULT 12
US-09-022-260-1
; Sequence 1, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-09-022-260-1

Alignment Scores:
Pred. No.: 1.5e-06 Length: 3288
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
Best Local Similarity: 20.4% Mismatches: 192
Query Match: 4.8% Indels: 207
DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-09-022-260-1 (1-3288)

Qy 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAAACCTGACCCCGCTTCCCAAAAAACATCTATATCAATCTTAGTGTTCCTCTACC 375
Qy 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGCGAGNATAGTTCCTCTGTTGATGTTGAG---TGGACCTGCGACAGATGCC 432
Qy 254 -----SergluArg 256
Db 433 AGCATCTGTACCTCGAGGGTGCAGAGTGTCCGTCTCGAGCTGAACACCAATGACGG 492
Qy 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTCTCAAGTTTC---CAGTTTCTCTCCATGCTGCAGCATCACCGTAAAGCGGTGGCG 549
Qy 275 IleAlaArgLeuArg---ValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
Db 550 TTTTCCTTCAGCCACTTTGTGTGATGCTTGGC----- 582
Qy 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTATGAAGTGACTGTT-----CACCACCTG 612
Qy 314 ValProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCCATCCCTGTATGGGGACCAACCAAAATCCA----- 652
Qy 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345

653 -----AGATCATCTTTGTGCTGAGCAGCAGCAAGATGAAGATGACTACCTCA 705
346 -----TTPGlulysValGlnLeuG1 352
706 TGGTGAGCTCAGCGACGCTTTGGGATCCCAACATCACTGTGGAGACCTTGGACACACAG 765
352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe 372
766 CATCTGGAGTGG----- 778
372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerglyCy 389
779 -----ACTTCACCTGTGGAATGAATCCACCCCTACCAGGTCTGTG 819
389 sThrProLeu---ProSerMetalaserThrArgAlaAlaArgLeuGluGluLeuLe 408
820 CTGGAAGTTTCTCCGACTCAGAGAACACACAGCTGCTTTGATGTCGTGTAACAATAATTT 879
408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLe 428
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428 u---TrpAlaCys----- 431
939 TCACTGTGTGCTGCCATCACCACGTGCAGGTCCAGCCCTTCTTCAGCAGCTGCCTAAATGA 998
431 ----- 431
999 CTGTTTGAGACACGCTGTGATGTGCCCTGCCAGTAATCTCAATATACCAGATTCCTCAA 1058
432 -ProMetAspLysTrpIleHisArgArgTrpVal-----LeuValTrpLeuAlaCysLe 449
1059 GCCAGTTGCAGACTACATT---CCCCTGTGGGTATGCGCTCATCACATCATCGCCAT 1115
449 uLeuLeuAlaAlaAlaLeuPhePheLeu-----LeuLeuLysLy 463
1116 TCTGTGTGGGATCTGTCTCATGTGTGATCATCTGTATGATCCTGTGAGGCTTTCTGGCGC 1175
463 sAspArgArgLysAlaAlaArgGlySer----- 472
1176 CGATCAAGAGAAACATGTGTGATGACTCCAAATCAATGGCATCTTGCCTGAGCAGACCT 1235
473 -----ArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaG1 485
1236 GACTCCCCACCCCTGAGGCCAGGAGGTCTGATCGTCTACTCTGCGCCACACCCCT 1295
485 YTrpGluArgLeuValGlyAlaLeuAlaSerAlaLeu---SerglnMetProLeuArgVa 504
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1356 AGCCCTTGACCTCTCGAAGAGCAGGTTATCTCTGAGGTGGGGTTCATGACCTGGGTGAG 1415
524 sHisGlnArgArgArgIleLeuGlnGlyValValIleLeuLeuPheSer----- 542
1416 CCGACAGAAGCAGAGATGTGTGAGAGCAACTCCAAATCATCTCTGTGTTCGCGAGG 1475
543 -----ProAlaAlaValAlaGlnCy 549
1476 CACCAAGCAAGTGGAAAGCTATCTTGGGTGGGCTGAGCCTGCTCTCCAGCTACGGTG 1535
549 sGlnGlnTrpLeuGlnLeuGlnThrValGluProGlyProHisAspAlaLeuAlaTr 569
1536 TGACCACTGG-----AAGCCTGCT---GGGACCTTTTTCATCTGCAGC 1574
569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyVa 589
1575 CATGAACATGATCTCTCCAGACTTCAAGAGCCAGCGCTGCTTGGCAGCTACCTGTTGTTG 1634
589 lTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLe 609
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Tue Aug 22 11:34:35 2006

Db 1635 CTACTCAGTGGGACATCTGTAGTGGAGGGATGTCCTCCGACCTCTTCAACATCACCTCCAG 1694
Qy 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
Db 1695 GTACCCACTCATGGACAGATTGTGAGAGGTTTACTTCCGGATCCAGGACCTGGAGATGTT 1754
Qy 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
Db 1755 TGAACCCGGCGGATGCACCATGTACAGAGACTCACAGGGGACAAATTACTCTGCAGAGCCC 1814
Qy 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlap 659
Db 1815 TAGTGGCGGCGAGCTCAGGAGGCTGTGCTTAGTTCCAGGAGTGGCAAAACCCAGTCCCC 1874
Qy 659 ro 659
Db 1875 CG 1876
RESULT 13
US-09-022-259-1
; Sequence 1, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS

i LOCATION: 121..2715
US-09-022-259-1
Alignment Scores:
Pred. No.: 1.5e-06 Length: 3288
Score: 174.50 Matches: 119
Percent Similarity: 31.6% Conservative: 65
Best Local Similarity: 20.4% Mismatches: 192
Query Match: 4.8% Indels: 207
DB: Gaps: 26
US-10-719-202-2 (1-674) x US-09-022-259-1 (1-3288)
Qy 224 LysAsnLeuThr-----GlyProGlnAsnIleThrLeuAsn----- 235
Db 316 AAAARCTGACCCCGCTCTCCCAAAAACATCTATCAATCTTAGTGTCTCTCTACC 375
Qy 236 ---HisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp--- 253
Db 376 CAGCAGGAGATTAGTCCCTGTGTTCATGTTGAG---TGGACCTGCAGACAGATGCC 432
Qy 254 -----SerGluArg 256
Db 433 AGCATCTCTTACCTCGAGGGTGCAGAGCTCTCGTCTGCAGCTGAACCAATGAGCGG 492
Qy 257 -----ValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrpHis 274
Db 493 CTGTGTGTCAAGTTC---CAGTTTCTGTCCATCTGCAGCATCACCGTAAAGCGGTGGCGG 549
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Db 550 TTTTCTTTCAGCCACTTGTGTGTAGATCTCTGGC----- 582
Qy 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
Db 583 CAGGAGTATGAGTGACTGTT-----CACCACTG 612
Qy 314 ValProProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
Db 613 CCGAAGCCCATCTGTATGGGACCCCAACACCAAAATCCA----- 652
Qy 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
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Qy 346 -----TrpGluLysValGlnLeuG1 352
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Db 766 CATCTGCGAGTGG----- 778
Qy 372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389
Db 779 -----ACTTCACTGTTGGAATGAATCCACCCCTTACCAGGTCTCTG 819
Qy 389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeu 408
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Qy 408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLe 428
Db 880 GCGCCCGCAGGCAAGAAGTTCATCAGCAGCTAATGTCACTTC-AC'TCTAAGCAAGT 938
Qy 428 u---TrpAlaCys----- 431
Db 939 TCACTGTGTGCTGCCATCACCGTGCAGGTCCAGCCCTTCTTCAGCAGTGCCTTAATGA 998
Qy 431 ----- 431
Db 999 CTGTTTGAGACACGCTGTGCTGTGCTGCTGCCAGTAAATCTCAATATCACACAGTTCCTCAA 1058

550 TTTTCCTTCAGCCACTTTGTGTAGATCCTGGC----- 582
294 LeuProGlyIysValThrLeuCyTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
583 CAGGAGTATGAAGTGACTGTT-----CACCACCTG 612
314 ValProProValProGlnLysAsn-AlaThrValAsnGluProGlnAspPheGlnLeuVa 333
613 CCGAAGCCCATCCCTGTGATGGGAGCCCAACACAAATCCA----- 652
333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
653 -----AGATCATCTTTGTGCTGACTGTGAGGACAGCAAGATGAAGATGACTACCTCA 705
346 -----TrpGluLysValGlnLeuG1 352
706 TGCCTGAGCTCAGGAGCCTTTGGATCCCAACATCACTGTGGAGACCTTGGACACAG 765
352 nAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMetLeuLeuValGluMe 372
766 CATCTGCCAGTGG----- 778
372 tLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluPro-----SerGlyCy 389
779 -----ACTTCACCTGTGGATGAATCACTCCCTTACCAGTCTCTG 819
389 sThrProLeu---ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLe 408
820 CTGGAAAGTTCTCCGATCAGACAGAACACAGCTGCTTTGATGCTGTTAAACAATATT 879
408 uGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLe 428
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428 u---TrpAlaCys----- 431
939 TCACTGGTGTGCTGCCATCACACGTGAGTCCAGGTCAGCCCTTCTCAGCAGCTGCTAAATCA 998
431 ----- 431
999 CTGTTTGGACAGCTGTGACTGTGCTGCCCTGCCAGTAATCTCAAAATACACAGTTTCCCAA 1058
432 -PrometAspLysTyrlleHisArgTrpVal-----LeuValTrpLeuAlaCysLe 449
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1236 GACTCCCCCCTGAGGCCCCAGGAGGTCTGATCTGATCATCTGTATGACCTGGAGGCTTCTGGCGC 1295
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524 sHisGlnArgArgIleLeuGlnGlyValValIleLeuLeuPheSer----- 542
1416 CCGACAGAACGAGAGATGGTGGAGCACTCCAAATCATCTCTGTGTTCCCGAGG 1475
543 -----ProAlaAlaValAlaGlnCy 549
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Db 1536 TGACCACTGG-----AAGCCTGCT---GGGACCTTTTCACTGCAGC 1574
QY 569 pLeuSerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyValGlyVa 589
Db 1575 CATGAACATGATCTCTCCAGACTTCAAGAGGCGCAGCCTCTTCCGACCTACCTGTTTGG 1634
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Db 1635 CTACTTCAGTGGCATCTGTAGTGAGAGGATGTCCTCCGACCTCTTCAACATCACCTCCAG 1694
QY 609 uPheSerLeuPro-ThrGlnLeuProAlaPheLeuAspAlaLeuGln----- 624
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QY 625 -----GlyGlyCysSer-----ThrSerAlaGlyArgProAlaAspArgValG 639
Db 1755 TGAACCGCGCGGATGCACCATGTCAAGAGGCTCACAGGGGACAAATTACCTGCAGAGCCC 1814
QY 639 luArgValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSerSerGluAlaP 659
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US-09-549-679-1
; Sequence 1, Application US/09549679
; Patent No. 6680057
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; Spriggs, Melanie
; Fangelow, William
; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,679
; FILING DATE: 14-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Mouse
 STRAIN: HVS13 receptor
 FEATURE:

NAME/KEY: CDS
 LOCATION: 121..2715
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-549-679-1

Alignment Scores:

Pred. No.: 1.5e-06 Length: 3288
 Score: 174.50 Matches: 119
 Percent Similarity: 31.6% Conservative: 65
 Best Local Similarity: 20.4% Mismatches: 192
 Query Match: 4.8% Indels: 207
 DB: 3 Gaps: 26

US-10-719-202-2 (1-674) x US-09-549-679-1 (1-3288)

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DB 433 AGCATCTGTACCTCGAGGTGCAGAGCTGTCGTCCTGCAGCTGAACACCAATGAGCG 492
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DB 493 CTGTGTGTCAAGTTC---CAGTTTCTGTCCTGATGTCAGCATCACCGTAAGCGGTGGCG 549
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QY 294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
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QY 333 lAlaGlyHisProAsnLeuCysValGlnValSerThr----- 345
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QY 346 -----TrpGluLysValGlnLeuG 352
DB 706 TGGCTGAGCTCAGGACGCTTTGGGATCCCAACATCACTGTGGAGACCTTGGACACACAG 765
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DB 766 CATCTCGAGTGG----- 778
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DB 820 CTGGAAAGTTTCTCCACTCAGAGAACCAACAGCTGCTTTGATGCTGTTAAACAATATT 879
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 Job time : 386 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2006, 09:11:08 ; Search time 269 Seconds
(without alignments)

6007.995 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

Sequence: 1 MPVSWFLSLALGRNPVWS.....SSRAGCCCEWDIGPCTTLE 674

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCHI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowum62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRAN MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abes03p
-USER=US10719202 @CGN_1_1_316 @runat_16082006_095640_13429 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA_New:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2339	64.9	2380	8	US-11-311-555-13
3	2339	64.9	2380	8	US-11-311-561-13
4	2339	64.9	2380	8	US-11-101-316-161
5	2339	64.9	2380	8	US-11-311-554-13
6	2339	64.9	2380	9	US-11-376-673-161
7	1971	54.7	2350	8	US-11-293-697-1517

c	8	1350	37.4	1373	8	US-11-266-748A-15241	Sequence 15241, A
c	9	1350	37.4	1373	8	US-11-266-748A-64946	Sequence 64946, A
c	10	1350	37.4	1373	8	US-11-266-748A-67778	Sequence 67778, A
c	11	1096.5	30.4	1864	8	US-11-293-697-313	Sequence 313, App
c	12	916.5	25.4	757	8	US-11-266-748A-218328	Sequence 218328,
c	13	916.5	25.4	757	8	US-11-266-748A-239031	Sequence 239031,
c	14	897.5	24.9	1000	8	US-11-266-748A-239048	Sequence 239048,
c	15	897.5	24.9	1000	8	US-11-266-748A-344477	Sequence 344477,
c	16	870.5	24.1	1000	8	US-11-266-748A-293049	Sequence 293049,
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c	18	774	21.5	1061	8	US-11-266-748A-361314	Sequence 361314,
c	19	774	21.5	1061	8	US-11-266-748A-387554	Sequence 387554,
c	20	774	21.5	1061	8	US-11-266-748A-444693	Sequence 444693,
c	21	765	21.2	885	8	US-11-266-748A-361313	Sequence 361313,
c	22	765	21.2	885	8	US-11-266-748A-387553	Sequence 387553,
c	23	765	21.2	885	8	US-11-266-748A-403105	Sequence 403105,
c	24	758.5	21.0	1000	8	US-11-266-748A-403105	Sequence 403105,
c	25	758.5	21.0	1000	8	US-11-266-748A-474151	Sequence 474151,
c	26	735	20.4	923	8	US-11-266-748A-261876	Sequence 261876,
c	27	735	20.4	923	8	US-11-266-748A-322393	Sequence 322393,
c	28	729	20.2	1144	8	US-11-266-748A-361315	Sequence 361315,
c	29	729	20.2	1144	8	US-11-266-748A-387555	Sequence 387555,
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c	31	724.5	20.1	681	8	US-11-266-748A-186516	Sequence 186516,
c	32	724	20.1	810	8	US-11-266-748A-364147	Sequence 364147,
c	33	724	20.1	810	8	US-11-266-748A-388229	Sequence 388229,
c	34	724	20.1	810	8	US-11-266-748A-447526	Sequence 447526,
c	35	651	18.1	1156	8	US-11-266-748A-480243	Sequence 480243,
c	36	597.5	16.6	571	8	US-11-266-748A-6434	Sequence 6434, Ap
c	37	596	16.5	548	8	US-11-266-748A-364146	Sequence 364146,
c	38	596	16.5	548	8	US-11-266-748A-388228	Sequence 388228,
c	39	596	16.5	548	8	US-11-266-748A-447525	Sequence 447525,
c	40	566	15.7	500	8	US-11-266-748A-364072	Sequence 364072,
c	41	566	15.7	500	8	US-11-266-748A-447451	Sequence 447451,
c	42	550.5	15.3	939	8	US-11-266-748A-177972	Sequence 177972,
c	43	543.5	15.1	494	8	US-11-266-748A-62257	Sequence 62257, A
c	44	507.5	14.1	620	8	US-11-266-748A-42371	Sequence 42371, A
c	45	338.5	9.4	2221	9	US-11-253-200-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-10-196-749-597

Sequence 597, Application US/10196749

Publication No. US20060094864A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Deenover, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: F3430R1C340

CURRENT APPLICATION NUMBER: US/10/196,749

PRIOR FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: 10/052586

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
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 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
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 ; ORGANISM: Homo Sapien
 US-10-196-749-597

Alignment Scores:
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 Query Match: 64.9% Indels: 34
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US-10-719-202-2 (1-674) x US-10-196-749-597 (1-2380)

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 QY 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisHisGlnArgArgIleLeuGlnGlu 533
 DB 1847 CTGAGCGCGAGGGGCGCGGT 1906
 QY 534 GlyValValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
 DB 1907 GCGGCGGT 1966
 QY 554 GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu 570

```
Db 1967 CAGGATGGGTGTCGGGGCGCGACGGCCCGCAGACGGCTTCGGCGCTCGCTC 2026
Qy 571 SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyr 590
Db 2027 AGTCGTGCTGCGCGACTTCTTCAGGGCGGGCGCGCGCGAGCTACGTGGGGCGCTGC 2086
Qy 591 PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe 610
Db 2087 TTCACAGAGGTGCTCCACCGGACGGGTATCCCGCCCTTTTCGCGACCGGTCCGCTTC 2146
Qy 611 SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSer 630
Db 2147 ACATCGCCCTCCCACTGCCAGACTTCTCGGGGCGCTTCGACGAGCTCGCGCCCCCGCT 2206
Qy 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
Db 2207 TCGGGCGGCTCCCAAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGAT 2266
Qy 651 SerCys-----ThrSerSerSerGluAlaProGly 660
Db 2267 AGCTACTTCATCCCGCGGAGCTCCCGCGCGGGA 2302
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RESULT 2

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US-11-311-555-13
; Sequence 13, Application US/11311555
; Publication No. US2006008916A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/11/311,555
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 13
; LENGTH: 2380
; TYPE: DNA
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; ORGANISM: Homo Sapien
US-11-311-555-13
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Alignment Scores:

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Pred. No.: 4,53e-171 Length: 2380
Score: 2339.00 Matches: 459
Percent Similarity: 75.9% Conservative: 66
Best Local Similarity: 66.3% Mismatches: 133
Query Match: 64.9% Indels: 34
DB: 8 Gaps: 7
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US-10-719-202-2 (1-674) x US-11-311-555-13 (1-2380)
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Qy 1 MetProValSerTrpPheLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 233 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 293 CTGGAGAGGCTTGTGGGGCTTCAGGACGCTACCCACTGCTCTCGGGCCTCTCCTGCCG 352
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 353 CTCTGGACAGTCACATACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 412
Qy 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 413 CTGGCGCTTACGCACCTTCAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
Qy 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
Db 473 GACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532
Qy 101 Glu-----AlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSer 116
Db 533 GATGAGGAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGAAATGCTCT 592
Qy 117 LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProIleAlaArgCysAlaLeuLeu 136
Db 593 CTCAGGCGCCAGCTCGTGTCTCTTCCAGGCTTACCTACTGCCCGCTGGTCTGCTGCTG 652
Qy 137 GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe 156
Db 653 GAGGTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
Qy 157 AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrThrLysProArg 176
Db 713 GACTGCTTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772
Qy 177 TyrGlnLysGluLeuAsnLeuThrGlnGlnLeuPro----- 188
Db 773 TACGAGAGGAACTCAACCCACACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
Qy 189 ---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe 207
Db 833 GCAGATGGTGACAAACGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
Qy 208 LeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThr 227
Db 893 TCCTGTACTTGGAAATCAGGTTCAGGGCCCCCCCCCCCCCGGGTGGCACAACAAACCTG 952
Qy 228 GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal 247
Db 953 GGACCCGACATCATTTACCTTGAACCAACACAGACCTGCTGCTGCTGCTGCTGCTGCTG 1012
Qy 248 TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly 267
Db 1013 TGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTTCAGGGAGGAGCCCG 1072
Qy 268 AlaHisArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln 287
Db 1073 GCACACCAAGAACCTCTGGCAAGCCGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1132
```


APPLICANT: Gurney,Austin L.
 APPLICANT: Wood,William I.
 TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
 TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
 FILE REFERENCE: P3230R1C17C1
 CURRENT APPLICATION NUMBER: US/11/101,316
 CURRENT FILING DATE: 2005-04-06
 PRIOR APPLICATION NUMBER: 10/063526
 PRIOR FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: 10/006867
 PRIOR FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: 09/380137
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: 1999-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 161
 LENGTH: 2380
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-11-101-316-161

Alignment Scores:
 Pred. No.: 4,53e-171 Length: 2380
 Score: 2339, 00 Matches: 459
 Percent Similarity: 75.9% Conservative: 66
 Best Local Similarity: 66.3% Mismatches: 133
 Query Match: 64.9% Indels: 34
 Gaps: 7

DB:

US-10-719-202-2 (1-674) x US-11-101-316-161 (1-2380)

QY	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer	20
DB	233	ATGCCTGTGGCCCTGGTCTTCCTGTCTTGCACTTGGCGCCGAGCCAGTGGCTTTCT	292
QY	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
DB	293	CTGGAGAGGCTGTGGGCCCTCAGGACGCTACCACACTCTCTCGGGGCTCTCTCGCCG	352
QY	41	LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
DB	353	CTCTGGGACAGTAGCATATCTGCTGCTGGCGGACATCGTGCCTCTCGGGCCCGCTG	412
QY	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
DB	413	CTGGCGCCCTACCGACCTCGCAGACAGAGCTGGTGTCTGAGGTGCCAGAAGGAGACCGA	472
QY	81	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
DB	473	GACCTCTGTCTGGTGTGGCTGTCCAATTGGCGCGTGCATGGGCACTGGGAAGAGCTGAA	532
QY	101	Glu-----AlaGlyIysSerAspSerGluLeuGlnGlnSerArgAsnAlaSer	116
DB	533	GATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCT	592
QY	117	LeuGlnAlaGlnValValLeuSerPheGlnAlaTyrrProIleAlaArgCysAlaLeuLeu	136
DB	593	CTCAGGCCCAAGTCTGTCTCTCTTCCAGGCCCTACCTACTGCCCGCTGCGTCTCTGCTG	652
QY	137	GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe	156
DB	653	GAGGTGCAAGTGTCTGTGGCTGTGTCAGATTGGTCAGTCTGTGGGCTCTGTGGTATAT	712
QY	157	AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrrThrIysProArg	176
DB	713	GACTGCTTCGAGGCTGCCCTAGGAGTGAAGTACGAATCTGTCTTACTATCATGACCCAGG	772
QY	177	TyrGlnIysGluLeuAsnLeuThrGlnGlnLeuPro-----	188

Db	1947	CTGAGCGGCAGGGGCCGTGGCTTGGTTTCACGCGCAGCGCGCCACAGACCTCTCAGGAG	1906
Qy	534	GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnTrpLeu	553
Db	1907	GGCGCGTGTTGGTCTTGGCTCTCTCTCCCGGTGCGGTGTGCAGCGAGTGGCTA	1966
Qy	554	GlnLeuGlnThrValGluPro-----GlyProHisaspAlaLeuAlaAlaTrpLeu	570
Db	1967	CAGATCGGGGTGTCGGCGCCCGGGCGCACGCGCCCGCACACGCTTCCGCGCTCGCTC	2026
Qy	571	SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyValGlyValTyx	590
Db	2027	AGCTGCGTGTGTCGCGACTCTTTCAGAGGCGCGGCGCGGACGTACGTGGGGCTTCG	2086
Qy	591	PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe	610
Db	2087	TTCGACAGGCTGCTCCACCGGACCGCGGTACC CGCCCTTTTCCGACCGGTGCGCTCTC	2146
Qy	611	SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer	630
Db	2147	ACA CTGCCCTCCCAACTGCCAGACTTCTTCGGGGCGCTTCGACGACGCTCGCGCCGCGT	2206
Qy	631	AlaGlyArgProAlaAspArgValGluArgValThrglnAlaLeuArgSerAlaLeuAsp	650
Db	2207	TCCGGCGGCTCCNAG	2266
Qy	651	SerCys-----ThrSerSerSerGluAlaProGly	660
Db	2267	AGCTACTTCCATCCCCCGGGGACTCCCGCGCGCGGA	2302
RESULT 5			
US-11-311-554-13			
; Sequence 13, Application US/11311554			
; Publication No. US20060134755A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Chen, Jian			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul			
; APPLICANT: Grimaldi, Christopher			
; APPLICANT: Gurney, Austin			
; APPLICANT: Li, Hanzhong			
; APPLICANT: Hillan, Kenneth			
; APPLICANT: Tumas, Daniel			
; APPLICANT: VanLookeren, Menno			
; APPLICANT: Vanden, Richard			
; APPLICANT: Watanabe, Colin			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William			
; APPLICANT: Yansura, Daniel			
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF			
; FILE REFERENCE: P1381R1C1P1 (US)			
; CURRENT APPLICATION NUMBER: US/11/311,554			
; CURRENT FILING DATE: 2005-12-20			
; PRIOR APPLICATION NUMBER: US/09/747,259			
; PRIOR FILING DATE: 2000-12-20			
; PRIOR APPLICATION NUMBER: US 09/311,832			
; PRIOR FILING DATE: 1999-05-14			
; PRIOR APPLICATION NUMBER: US 60/172,096			
; PRIOR FILING DATE: 1999-12-23			
; PRIOR APPLICATION NUMBER: PCT/US99/31274			
; PRIOR FILING DATE: 1999-12-30			
; PRIOR APPLICATION NUMBER: US 60/175,481			
; PRIOR FILING DATE: 2000-01-11			
; PRIOR APPLICATION NUMBER: PCT/US00/04341			
; PRIOR FILING DATE: 2000-02-18			
; PRIOR APPLICATION NUMBER: PCT/US00/05841			
; PRIOR FILING DATE: 2000-03-02			
; PRIOR APPLICATION NUMBER: US 60/191,007			
; PRIOR FILING DATE: 2000-03-21			
; PRIOR APPLICATION NUMBER: PCT/US00/07532			

QY 248 TrpSerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGly 267
Db 1013 TGGCTCTGGAAACCTGATCTCGTTAGACCAACATCTGCCCCCTTCAGGAGGACCCCCCG 1072
QY 268 AlaHisArgenLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGln 287
Db 1073 GCACACAGAACCTCTGCGAACCGCCGCGACTGCGACTGTGACCTCGACCCCTGCAGAGCTGGCTG 1132
QY 288 LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGln 307
Db 1133 CTGAGCGCACCTGCTGCTGCCCGCAGAGCGGCACTGTGCTGCGGCGCTCGGGTGGG 1192
QY 308 SerProCysGlnProLeuValProValProGlnLysAsnAlaThrValAsnGluPro 327
Db 1193 GACCCCTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAACGTCATCTGTGGACAGGTT 1252
QY 328 GlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu 347
Db 1253 CTCGAGTTCCTATTCGTAAGGCCACCTTAACCTCTGTGTTCAAGTGAACAGCTCGGAG 1312
QY 348 LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspMet 367
Db 1313 AAGCTGCAGCTGCAGGAGTGTGTGGCTGACTCCCTGGGGCCCTCTCAAGAGCAATGTG 1372
QY 368 LeuLeuValGluMetLysThrGlyLeuAsnAnThrSerValCysAlaLeuGluProSer 387
Db 1373 CTACTGTTGGAGACAGCGCCCGCCCGACAGACAGATCCCTCTGTGCTTGGACCCAGT 1432
QY 388 GlyCysThrProLeuProSerMetAlaSerThrAlaAlaArgLeuGlyGluLeu 407
Db 1433 GGCTGTACTTACTACCCAGCAAGCCTCCAGAGCGCAGCTCGCTTGGAGTACTTA 1492
QY 408 LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspMetGlySer 427
Db 1493 CTACAAGACTGCAGTCAGCCAGCTGTCTGACGTATGG---GACATGACTTGGAGCG 1549
QY 428 LeuTrpAlaCysProMetAspLysTrpIleHisArgArgTrpValLeuValTrpLeuAla 447
Db 1550 CTATGGGCTGCCCATGGACAAATACATCCAGCGCTGGGCCCTCGTGTGGCTGGCC 1609
QY 448 CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLysLysAspArgLys 467
Db 1610 TGCCTACTCTTTCGCGCTGGCTTCCCTCATCTCTTCTCAAAAGATACCGGAAA 1669
QY 468 -----AlaAlaArgGlySerArg 473
Db 1670 GGGTGGCTGAGGCTCTTGAACAGGAGCTCCGCTCGGGGGCGCGCCAGGGGC---CGC 1726
QY 474 ThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTrpGluArgLeuValGlyAlaLeu 493
Db 1727 GCGCTCTGCTCTTACTCAGCGCATGACTCGGGTTTCAGCGCCTCGTGGGCGCCCTG 1786
QY 494 AlaSerAlaLeuSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgArgGlu 513
Db 1787 GCGTGGCCCTGTGCCAGCTCGCCCTCGCGGTGGCCGTAGACTGTGGAGCCCTCGTGA 1846
QY 514 LeuSerAlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgIleLeuGlnGlu 533
Db 1847 CTGAGCGCGAGGGCCCGTGGCTTGTTCACGCGCAGCGCGCCAGACCTCGCAGGAG 1906
QY 534 GlyGlyValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLeu 553
Db 1907 GCGGCGTGGTGGTCTTCTCTCTCCCGTGGGTGGCGTGTGACGAGTGGCTA 1966
QY 554 GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu 570
Db 1967 CAGATGGGGGTGTCGGGCGCCGGGCGCACGCCCGCGCACGCGCTTCGCGCCCTCGCTC 2026
QY 571 SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTrpValGlyValTyr 590
Db 2027 AGCTGCGTGTGCGCGACTTCTTTCAGGGCGCGGCGCCGCGCAGCTAGTGGGGCGCTGC 2086
QY 591 PheAspGlyLeuLeuHisArgSerValProSerProPheArgValAlaProLeuPhe 610

Db 2087 TTCGACAGGCTCTCCACCCGACCGGTACCCGCCCTTTCCGACCGTGCCTCTTC 2146
QY 611 SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer 630
Db 2147 ACATGCTCTCCCACTTCCGACATTCCTTGGGGCCCTGCAGCAGCTCGCGCCGCT 2206
QY 631 AlaGlyArgProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp 650
Db 2207 TCCGGCGCGCTCCAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCAGCCCTGGAT 2266
QY 651 SerCys-----ThrSerSerSerGluAlaProGly 660
Db 2267 AGTACTTTCATCCCGGGGACTCCCGCGCCGGA 2302
RESULT 6
US-11-376-673-161
; Sequence 161, Application US/11376673
; Publication No. US20060160186A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
; TITLE OF INVENTION: LUNG TUMOR
; FILE REFERENCE: P3230R1C165C
; CURRENT APPLICATION NUMBER: US/11/376,673
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/063742
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 161
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-376-673-161
Alignment Scores:
Pred. No.: 4,536-171 Length: 2380
Score: 2339.00 Matches: 459
Percent Similarity: 75.9% Conservative: 66
Best Local Similarity: 65.3% Mismatches: 133
Query Match: 64.9% Indels: 34
DB: 9 Gaps: 7
US-10-719-202-2 (1-674) x US-11-376-673-161 (1-2380)
QY 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValValSer 20
Db 233 ATGCTGTGCCCTGGTCTTCTGTCTTGGCACTGGGCCGAAGCCAGTGTCTTCT 292
QY 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db 293 CTGGAGAGCTTGTGGGGCTTCAGGACGCTACCCTGTCTCCGGGCTCTCTCTGCGC 352
QY 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 353 CTCTGGACAGTGACATCTCTGCTGCTGGGACATCGTGGGCTCTCTCGGGCCCGTG 412
QY 61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
Db 413 CTGGCGCTACGCACTTCGACAGCAGAGCTGTGTAGGTGTCAGAGGACCGACTGT 472
QY 81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100

Db		473	GACCTCTGTCGTGGCGTGTGCCACTTGTGGCCGCTGCATGGGCACCTGGGAAGAGCCTTGAA	532
Qy		101	Glu-----AlaGlySerAspSerLeuLeuGlnGlnSerArgAsnAlaSer	116
Db		533	GATGAGGAAAAGTTTGGGAGGACGAGTCACTCAGCGGTGGAGAGCCTTAGGAATGCCTCT	592
Qy		117	LeuGlnAlaGlnValValLeuSerPheGlnAlaTrpProIleAlaAraCysAlaLeuLeu	136
Db		593	CTCAGAGCCCAGAAGTCGTGCTCTCTCCAGGCTACCCTACTGTGCCCGCTGGCTCTGCTG	652
Qy		137	GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe	156
Db		653	GAGGTGCAAGTGCCTGTGCCCCGTGGCAGTTGGTCAGTCTGTGGGCTCTGTGGTAATAT	712
Qy		157	AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTyrrLysProArg	176
Db		713	GACTGCTTCGAGGCTGCCCTAGGAGGTAGGTTACGAATCTGGTCTTATATACTCAGCCCCAGG	772
Qy		177	TyrGlnIysGluLeuAsnLeuThrGlnGlnLeuPro-----	188
Db		773	TACGAGAAGGAACCTCAACACACACAGCAGCTGCCTGCCCTGGCTCAACGTTGCA	832
Qy		189	--AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGlnAspPheSerPhe	207
Db		833	GCAGATGGTGACAACGTCATCTGGTCTGTGAATGCTCTGAGGAGCAGCACTTCGGCCTC	892
Qy		208	LeuLeuTyrrLeuArpGProValProAspAlaLeuLysSerLeuTyrrLysAsnLeuThr	227
Db		893	TCCCTGTACTGGAATCAGGTCACGGGCCCCCAAACACCCGGTGGCACAAAAACCTGACT	952
Qy		228	GlyProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal	247
Db		953	GGACCGCAGATCATATTACCTTGAACACACAGACCTGGTTCCCTGCCCTCTGTATTAGGTG	1012
Qy		248	TrpSerLeuGluProAspSerGluArgValGluPheCysProPheAraGluAspProGly	267
Db		1013	TGGCCTCTGGAACTGACTCCGTTAGACAGAACATCTGCCCTCTCAGGAGAGCCCCCGC	1072
Qy		268	AlaHisArgAsnLeuTrpHisIleAlaAraGluArgValLeuSerProGlyValTrpGln	287
Db		1073	GCACACAGAACCTCTGGCAAGCCGCCGACTGGCAGTGTGACCTTCGACGCTGGAGCTGGCTG	1132
Qy		288	LeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGln	307
Db		1133	CTGAGCGACCGTCTGCTGCCCGCAGAACGGCAGCTGTGCTGGCGGGCTCCGGGTGGG	1192
Qy		308	SerProCysGlnProLeuValProProValProGlnIysAsnAlaThrValasnGluPro	327
Db		1193	GACCCCTGCCAGCCACCTGGTGTCCACCCCTCTCTCCGGAGAACGTCATCTGGCAGCAAGTT	1252
Qy		328	GlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGlu	347
Db		1253	CTCGAGTTCCATTGCTGAAAGGCCACCTTAACCTCTGTGTTTCAAGGTGAACAGCTGGAG	1312
Qy		348	LysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMet	367
Db		1313	AAGCTGCAGCTGCAGGAGTGCTTGTGGCTGACTCCCTGGGGCCTCTCAAGACGATGTG	1372
Qy		368	LeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSer	387
Db		1373	CTACTGTTGGAGACACAGAGCCCCAGGACACAGATCCCTCTGTGCTCTGGAAACCCAGT	1432
Qy		388	GlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeu	407
Db		1433	GGCTGTACTTCATCCACGACGAAGCTCTCACAGAGGCAGCTGCCCTTGAGAGTACTTTA	1492
Qy		408	LeuGlnAspPheArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySer	427
Db		1493	CTACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGG--GACGATGACTTGGGAGCG	1549
Qy		428	LeuTrpAlaCysProMetAspLysTyrrIleHisArgArgTrpValLeuValTrpLeuAla	447
Db		1550	CTATGGCCCTGCCCAATGGAACAATATCAACAGCGCTGGGCCCTCTGTGTGCTGGCC	1609

Qy	448	CysLeuLeuLeuAlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys	467
Db	1610	TGCCTACTTTTGGCGTGCGCTTCCTCATCTCCTTCATAAAAGGATCACGCGAAA	1669
Qy	468	-----AlaAlaArgGlySerArg	473
Db	1670	GGGTGGCTGAGGCTCTTTGAACAAGACGTCGCTCGGGGGCGGCCGCAGGGGC---CGC	1726
Qy	474	ThrAlaLeuLeuHisSerAlaAspGIYValaGLYTyrGluArgLeuValGIYAlaLeu	493
Db	1727	GCGGCTCTGTCTCTTACTCAGCCGATCACTGGGTTCGAGCGCCTGTGTGGGCGCCCTG	1786
Qy	494	AlaSerAlaLeuSerGlnMetProLeuArgValaLaValaAspLeuTrpSerArgArgGlu	513
Db	1787	GCGTCGCCCTGTGCCAGCTGCGCTGCGCTGAGACCTGTGGAGCGGTGCTGAA	1846
Qy	514	LeuSerAlaHisGIYAlaLeuAlaTrpPheHisGlnArgArgArgIleLeuGlnGlu	533
Db	1847	CTGAGCGCAGGGGGCCGTGTGCTTTTCAGCGCAGCGCGGCCACAGACCCTGCAGGAG	1906
Qy	534	GlyGlyValValIleLeuLeuPheSerProAlaAlaValaGlnCysGlnGlnTrpLeu	553
Db	1907	GCGCGCGTGTGTGTGCTTCTTCTCCCGTGTGGTGTGCTGTGCAGCGAGTGTGCTA	1966
Qy	554	GlnLeuGlnThrValGluPro-----GlyProHisAspAlaLeuAlaAlaTrpLeu	570
Db	1967	CAGGATGGGTGTCTCGGGCCCGGGGCGCACGGCCCGCACGACGCTTCCGCGCTCGCTC	2026
Qy	571	SerCysValLeuProAspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyr	590
Db	2027	AGCTGCGTGTGCCCGCATCTTTCAGGGCGCGGCGCGCCGCGCAGTACGTGGGGGCGCTGC	2086
Qy	591	PheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAlaProLeuPhe	610
Db	2087	TTTCACAGGTGTCTCCACCGGAGCGGTACCGCCCTTTTCGCGACCGTGCOCGTCTTC	2146
Qy	611	SerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSer	630
Db	2147	ACATCGCTCTCCCACTTCCACAGATTCTGGGGGCGCTTCGACGAGCCTCGCGCCCGCGT	2206
Qy	631	AlaGlyArgProAlaArgArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAsp	650
Db	2207	TCCGGGCGGTCCAAGAGAGAGCGGCAAGTGTCCGGGCGCCTTCAGCAGCCCTGTGAT	2266
Qy	651	SerCys-----ThrSerSerSerGluAlaProGly	660
Db	2267	AGCTACTTTCATCCCCCGGGGATCTCCCGCGCCGGGA	2302

RESULT 7

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US-11-293-697-1517
; Sequence 1517, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1517
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1517

Alignment Scores:
Pred. No.: 1.25e-142 Length: 2350
Score: 1971.00 Matches: 413
Percent Similarity: 62.7% Conservative: 59

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Best Local Similarity: 54.8% Mismatches: 125
Query Match: 54.7% Indels: 157
DB: 8 Gaps: 11

US-10-719-202-2 (1-674) x US-11-293-697-1517 (1-2350)

QY	1	MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer	20
DB	209	ATGGCTGTGGCTGGTCTTGTCTGCTTGTGCTTGTGGCGAAGCCAGCTGTGCTTCT	268
QY	21	LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSerCysHis	40
DB	269	CTGAGAGGCTTGTGGGCGCTCAGACGCTACCCACTGCTCTCCGGGCGCTCTCTCCGCC	328
QY	41	LeuTrpAsp	43
DB	329	CTCTGGG-TGCCACCAAAATCTGGGCTTGGAAACAGCTTCAGCTCCACCAGCTCTCTCCA	387
QY	44	-----GlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal	60
DB	388	CACACAGACAGTGACATCTCTGCTGCTGGGACATCTGCTGCTGGGCGCCCGTG	447
QY	61	LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys	80
DB	448	CTGGCGCTTACACCTTGACAGACAGCTGTGTGTGAGTGTCCAGAGAGACTGACTGT	507
QY	81	AlaLeuArgValArgValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu	100
DB	508	GACCTCTGCTGGTGTGGCTGTCCACTTGGCGGTGCATGGGCACTGGGAAGACCTGAA	567
QY	101	Glu-----AlaGlySerAspSerGluLeuGlnGluSerArgAsnAlaSer	116
DB	568	GATGAGAAAAAGTTTCGAGGAGCAGCTGACTTAGGGGTGGAGGCTTAGGAATGCCTCT	627
QY	117	LeuGlnAlaGlnValValLeuSerPheGlnAlaTrpProIleAlaArgCysAlaLeuLeu	136
DB	628	CTCAGGCCCAAGTCGTGCTCTCTCCAGGCTACCTTACTGCCCGTGTGCTGCTGCTG	687
QY	137	GluValGlnValProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPhe	156
DB	688	GAGTGAAGTGGCTGTGCCCTGTGTGCAGTTGGTCACTCTGGGCTCTGTGGTATAT	747
QY	157	AspCysPheGluAlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArg	176
DB	748	GACTGCTTCGAGGCTGCCCTAGGAGTAGAGTACGAATCTGTCTTACTCAGCCGAG	807
QY	177	TyrGlnLysGluLeuAsnLeuThrGlnLeuPro-----	188
DB	808	TACGAGAGGAACCTCAACACACACAGCTGCTGCCCTGCCCTCAACGTGTCA	867
QY	189	---AspGlyAspAsnValLeuLeuThrLeuAspValSerGluGlnAspPheSerPhe	207
DB	868	GCAGATGTGACACAGTGTCATCTGTTCTGAATGCTCTCGAGGAGCAGCACTTCGGCCTC	927
QY	208	LeuLeuTyrLeuArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsn-----	225
DB	928	TCCCTGTATCTGAATCAGGTCAGGGCCCCCAAAAACCCCGGTGGCAAAAACCTGGTG	987
QY	225	-----	225
DB	988	AGGCTTCCCTTCCCAAGTCCATTCCTCACTGTAGGCGATGCTGTGCCAAGAGCGCAG	1047
QY	226	-----LeuThrGly	228
DB	1048	TGCCATATCAGAGAGATCCCTTGAAGAGACTCACCCCAAGCAGGAGAAATTCAGCTGGA	1107
QY	229	ProGlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuLysIleGlnValTrp	248
DB	1108	CCGCAATCATTTACCTTGAACACACAGACCTGGTTCCTGCTCTGTATTTCAGGTGG	1167
QY	249	SerLeuGluProAspSerGluArgValGluPheCysProPheArgGluAspProGlyVala	268
DB	1168	CTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTTCAGGGAGGACCCCGCGCA	1227


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411 heArgSerHisGlnCysMetGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpAlaC 431
125 -----CTATGG-----GACGATGACTTGGGAGCGCTATGGGCGCT 92
431 ysProMetAspLysTyrIleHisArgTrpValLeuValTrpLeuAlaCysLeuLeuL 451
91 GCGCCATGGACAAATACATCCACAGCGCTGGGCCCTCGTGTGGCTGGCGCTACTCT 32
451 euAlaAlaLeuPhePheLeuLeu 460
31 TTGGCGCTGGCGCTTTCCCTCATCTCTCTT 3

RESULT 9
US-11-266-748A-64946
; Sequence 64946, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64946
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (129)..(137)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-64946

Alignment Scores:
Pred. No.: 6.17e-95 Length: 1373
Score: 1350.00 Matches: 282
Percent Similarity: 67.3% Conservative: 35
Best Local Similarity: 59.9% Mismatches: 71
Query Match: 37.4% Indels: 85
DB: 8 Gaps: 7

US-10-719-202-2 (1-674) x US-11-266-748A-64946 (1-1373)
Qy 1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProValValSer 20
Db 181 ATGCTGTGGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 240
Qy 21 LeuGluArgLeuMetGluProGlnAspThrAlaArgCysSerLeuGlyLeuSer 40
Db 241 CTGAGAGAGCTTGTGGGCGCTCAGACGCTACCCACTCTCTCTCTCTCTCTCTCT 300
Qy 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60
Db 41 LeuTrpAspGlyAspValLeuCysLeuProGlySerLeuGlnSerAlaProGlyProVal 60

301 CTCTGGGACAGTACATCTCTGCTGCTGGGGACATCGTGCCTGCTCGGCGCCCGTG 360
61 LeuValProThrArgLeuGlnThrGluLeuValLeuArgCysProGlnLysThrAspCys 80
361 CTGGCGCCTACGCACCTGCAGACAGAGCTGTGTCTGAGGTGCAGAGGAGACCGACTGT 420
81 AlaLeuArgValArgValValValHisLeuAlaValHisGlyHisTrpAlaGluProGlu 100
421 GACCTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 459
101 GluAlaGlyLysSerAspSerGluLeuGlnGluSerArgAsnAlaSerLeuGlnAlaGln 120
460 -----GCTCTCTCTCCAGGCCCA 477
121 ValValLeuSerPheGlnAlaLysProIleAlaArgCysAlaLeuLeuValGlnVal 140
478 GTCTGTCTCTCTTCCAGGCCCTACCTTACTGCGCGCTGCTGCTGCTGCTGCTGCTG 537
141 ProAlaAspLeuValGlnProGlyGlnSerValGlySerAlaValPheAspCysPheGlu 160
538 CCTGCTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 597
161 AlaSerLeuGlyAlaGluValGlnIleTrpSerTrpThrLysProArgTyrGlnLysGlu 180
598 GCTGCCCTAGGAGTAGGTACGAATCTGTGTCTTATCTAGCCAGGTACGAGAGGAA 657
181 LeuAsnLeuThrGlnGlnLeuProAsp-----GlyAsp 191
658 CTCACGACACACAGCAGCTGCTGTC-CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
192 AsnValLeuLeuThrLeuAspValSerGluGlnAspPheSerPheLeuLeuTyrLeu 211
717 AACGTGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 773
212 ArgProValProAspAlaLeuLysSerLeuTrpTyrLysAsnLeuThrGlyProGlnAsn 231
774 -----TGG-----AATCAGACTGGACCGCAGATC 797
232 IleThrLeuAsnHisThrAspLeuVal-ProCysLeuCysIleGlnValTrpSerLeuG 251
798 ATTACCTTGAACACACAGAGCTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
251 uproAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAs 271
858 ACCTGACTCCGTAGGACGAAACATCTGCCCTTTCAGGAGGAGGAGGAGGAGGAGGAG 917
271 nLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaPr 291
918 CCTCTGGCAAGC-CGCGGACTGCGACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 976
291 o-CysCysLeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysG 311
977 GTTGTCTGCTGCCCGCAGAGCGGCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1036
311 lnProLeuValProProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheG 331
1037 AGCCACTGTGCTCCACCGCTTTCTGCGGAGATGTCTACTGTGGAC----- 1080
331 lnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTrpGluLysValGlnL 351
1081 -----GTGAACAGCTCGGAGAGTGCAGC 1105
351 euGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValG 371
1106 TGCAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1165
371 luMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrP 391
1166 AGACACGAGGCGCCCGAGGACACAGATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 1225
391 roLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluGluLeuLeuGlnAspP 411
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Db      1226  CACTACCACGAAAGCCCTCCACG----- 1248
Qy      411  heArgSerHisGlnCysMetGlnLeuTrpAenAspAsnMetGlySerLeuTrpAlaC 431
Db      1249  -----CTATGG-----GACGATGACTTGGGAGCGCTATGGGCT 1282
Qy      431  ysProMetAspLysTyrIleHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuL 451
Db      1283  GCCCCATGGAGCAAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCCTACTCT 1342
Qy      451  euAlaAlaAlaLeuPhePheLeuLeu 460
Db      1343  TTGGCGGTGGCCTTTCCTCATCTCCTT 1371

RESULT 10
US-11-266-748A-67778/c
; Sequence 67778, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 {319189}
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67778
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1237)..(1245)
; OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-67778

Alignment Scores:
Pred. No.: 6.17e-95 Length: 1373
Score: 1350.00 Matches: 282
Percent Similarity: 67.3% Conservative: 35
Best Local Similarity: 59.9% Mismatches: 71
Query Match: 37.4% Indels: 85
DB: 8 Gaps: 7

US-10-719-202-2 (1-674) x US-11-266-748A-67778 (1-1373)

Qy      1  MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAenProValValSer 20
Db      1193  ATGCCTGTGGCCTGGTCTTGCTGCTCTGGCACTGGGCGCAAGCCAGTGGTCCTTCT 1134
Qy      21  LeuGluArgLeuMetGluProGlnAaspThrAlaArgCysSerLeuGlyLeuSerCysHis 40
Db      1133  CTGGAGAGGCTTGTGGGGCGCTCAAGACGCTACCACCTGCTCTCGGGGCGCTCTCTCTGCCG 1074

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148 CACTACCCAGCAAGCCCTCCAGG-----126
411 heArgSerHisGlnCysMetGlnLeuTrpAsnAspMetGlySerLeuTrpAlaC 431
125 -----CTATGG---GACGATGACTTGGGAGCCCTATGGCCCT 92
431 ysProMetAspLysTrpHisArgArgTrpValLeuValTrpLeuAlaCysLeuLeuL 451
91 GCCCATGGACAAATATACATCACAGAGCGCTGGGCGCTCGTGGCTGGCTGCCTACTCT 32
451 euAlaAlaLeuPhePheLeuLeu 460
31 TTGGCGCTGCGCTTTCCCTCATCTCCTCT 3

RESULT 11
US-11-293-697-313
; Sequence 313, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 313
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-313

Alignment Scores:
Pred. No.: 3,7e-75 Length: 1864
Score: 1096.50 Matches: 254
Percent Similarity: 65.2% Conservative: 53
Best Local Similarity: 53.9% Mismatches: 108
Query Match: 30.4% Indels: 56
DB: 8 Gaps: 15

US-10-719-202-2 (1-674) x US-11-293-697-313 (1-1864)
QY 230 GlnAsnIleThrLeuAsnHisThrAspLeuValProCysLeuCysIleGlnVal-----247
DB 431 CAGACATTGTAATAAATCAT-----ATAGTATCTTAAATTTGCATACAAATACCATGG 484
QY 248 -----TrpSerLeuGlu-ProAs 253
DB 485 GAAAGGGTAAGTGGGACTGGGGTTGCAATTTTACAGAGGGTGGTGCATGTGAGAAAGGA 544
QY 253 pSer-----GluArgValGluPheCysProPheArgGluAspProGlyAl 268
DB 545 ATCTCTTTGAGAGGTTAGATGAGAGGGGAACCATGCTCGTAAGA-----590
QY 268 aHisArgAsnLeuTrpHisIleAlaArg-----LeuArgValLeuSerProGlyValTr 286
DB 591 -CATAAAAACAGCTTTAGGTGCTCAGAAGACGCTTTATACAGATGATCTCACAGGC---TG 646
QY 286 pGlnLeuAspAlaProCys-CysLeuProGlyLysValThrLeuCysTrpGlnAlaPro- 305
DB 647 GGGCAGAGAAAGA---TGTTAGTATCTTAATCACCAGCGCTTGAATCCACATCTGCCTC 703
QY 306 -----AspGlnSerProCysGlnProLeuValPro-----ProValProG 319
DB 704 AGGTCAGATTGAGTGCAGATTCCCAACCCCAACAGGCGCTTCTGTGCTGCCCATTT---759
QY 319 lnLysAsnAlaThrValAsnGluProGlnAspPheGlnLeuValAlaGlyHisProAsn- 338
DB 760 -----CTGGTCTTTCTGCTTGGCTTTTCTTTCTTAGTGGC---CCTAAC 805

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RESULT 12
 US-11-266-748A-218328/c
 ; Sequence 218328, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:


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Db 61 GTGTGGCCCTCTGGAACCTGACTCGCTTAGGACGAACTCTGCCCTTCAGGGAGGACCCC 120
Qy 267 GlyAlaHisArgAsnLeuTTPHisIleAlaArgLeuArgValLeuSerProGlyValTTP 286
Db 121 CGCGACACCAACAACTCTGCAAGCCGCCGACTGCGACTGCTGACCTCGACAGCTGG 180
Qy 287 GlnLeuAspAlaProCysLeuProGlyCysValThrLeuCysTTPGlnAlaProAsp 306
Db 181 CTGCTGGAGCACCCTGCTGCTGCCCGCAGAGGGCAGCTGTGCTGGCGGCTCCGGGT 240
Qy 307 GlnSerProCysGlnProLeuValProProValProGlnLysAsnAlaThrValAsnGlu 326
Db 241 GGGGACCCCTCCAGCCACTGCTGCCACCGTTCCTGGGAGAACGTCGCTGGACAAAG 300
Qy 327 ProGlnAspPheGlnLeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTTP 346
Db 301 GTTCTCGAGTTCCTTCTGTAAGGCCACCTTAACCTCTGTGTTCAGGTGAACAGCTCG 360
Qy 347 GluLysValGlnLeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAsp 366
Db 361 GAGAACTGCTGAGCTGAGAGTGTGTGGGCTGACTCCCTGGGGCTCTCTCAAAAGACGAT 420
Qy 367 MetLeuValGluMetLysThrClyLeuAsnAsnThrSerValCysAlaLeuGluPro 386
Db 421 GTGCTACTGTGGAGACACGAGGCCCGCCAGGACAAACAGATCCCTCTGTGCTTGGACCC 480
Qy 387 SerGlyCysThrProLeuProSerMetAlaSerThrArgAlaAlaArgLeuGlyGlu 406
Db 481 AGTGGCTGTACTTCACTACCCAGCAAGCCCTCCAGGAGGAGCTCGCTTGGAGATAC 540
Qy 407 LeuLeuGlnAspPheArgSerHisGlnCysMetGlnLeuTTPAsnAspAspAsnMetGly 426
Db 541 TTACTACAAGACCTGCAGTCAGCCAGTGTCTGCAGCTATGG--GACGATGACTTGGGA 597
Qy 427 SerLeuTTPAlaCysProMetAspLysTyrIleHisArgArgTTPValLeuValTTPLeu 446
Db 598 GCGCTATGGGCTGGCCCTGACCAAGCTTCCAGGAGGAGCTCGCTTGGGCTG 657
Qy 447 AlaCysLeuLeuAlaAlaLeuPhePheLeuLeuLysLysAspArgArg 466
Db 658 GCCTGCTACTCTTTGGCGCTCGCTTTCCTCATCTCTCTCTCAAAAGGATCACGCG 717
Qy 467 Lys 467
Db 718 AAA 720

RESULT 14
US-11-266-748A-293048
; Sequence 293048, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIORITY APPLICATION NUMBER: EP 04105479.2
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105482.6
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105483.4
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105507.0
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105485.9
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105484.2
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: US 60/662,276
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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 293048
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-293048

Alignment Scores:
Pred. No.: 3,86e-60 Length: 1000
Score: 897.50 Matches: 186
Percent Similarity: 74.2% Conservativeness: 27
Best Local Similarity: 64.8% Mismatches: 53
Query Match: 24.9% Indels: 21
DB: 8 Gaps: 5

US-10-719-202-2 (1-674) x US-11-266-748A-293048 (1-1000)
Qy 393 ProSerMetAlaSerThrArgAlaAlaArgLeuGlyGluLeuLeuGlnAspPheArg 412
Db 1 CCCAGCAAAAGCCTCCACGAGGCGAGCTGCGCTTGGAGAGTACTTACTACAAGACCTGCGAG 60
Qy 413 SerHisGlnCysMetGlnLeuTTPAsnAspAspAsnMetGlySerLeuTTPAlaCysPro 432
Db 61 TCAGGCCAGTGTCTGACGCTATGG--GACGATGACTTGGAGCGCTATGGGCTGCCCC 117
Qy 433 MetAspLysTyrIleHisArgArgTTPValLeuValTTPLeuAlaCysLeuLeuAla 452
Db 118 ATGACAAATACATCCACAGCGCTGGGCCCTCGCTGTGGCTGGCTGCTACTCTTTGGC 177
Qy 453 AlaAlaLeuPhePheLeuLeuLeuLysLysAspArgArgLys----- 467
Db 178 GCTGCGCTTTCCCTCATCTCTCTCTCAAAAGGATACGCGAAGGGTGGCTGAGGCTC 237
Qy 468 -----AlaAlaArgGlySerArgThrAlaLeuLeuLeu 478
Db 238 TTGAACAGGAGCTCGCTCGGGGGCGCGCGCAGGGGCG--CGCGCGCTCTGCTGCTC 294
Qy 479 HisSerAlaAspGlyAlaGlyTyrGluArgLeuValGlyAlaLeuAlaSerAlaLeuSer 498
Db 295 TACTCAGCCGATGACTCGGCTTTCAGGCGCTGTGGGGCGCTCGCGCTCGGCTGCTGCTG 354
Qy 499 GlnMetProLeuArgValAlaValAspLeuTTPSerArgArgGluLeuSerAlaHisGly 518
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Qy 576 AspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeu 595
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Qy 596 HisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGln 615
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Qy 616 LeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAla 635
Db 715 CTGCCAGACTTCTTGGGGGCGCTTGCAGCAGCGCTCGCGCGCGCGCTTCCGCGGCTCCAA 774
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REFERENCE	Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBLISHED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBLISHED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplex capillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBLISHED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBLISHED	
REFERENCE	5
AUTHORS	The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBLISHED	
REFERENCE	6
AUTHORS	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.
TITLE	Antisense transcription in the Mammalian Transcriptome
JOURNAL	Science 309, 1564-1566 (2005)
PUBLISHED	
REFERENCE	7
AUTHORS	The PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE	The Transcriptional Landscape of the Mammalian Genome
JOURNAL	Science 309, 1559-1563 (2005)
PUBLISHED	8 (bases 1 to 973)
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayaehida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.

FEATURES	URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/
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Best Local Similarity:	85.3%
Query Match:	33.4%
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Gaps:	1
DB:	6
US-10-719-202-2 (1-674) x AK040950 (1-973)	
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Db	880 ATCCACAGGCGCTGGCTCTAGTATGCTGGCTGCTACTCTTGGCTGGCGCTTTTC 821
QY	457 PhePheLeuLeuLeuLysLysAspArgArg-Lys- 467
Db	820 TTCTTCTCTCTTCTAAAGGACCGCAGGAAAGTGAGTGTTCCTCTGCTGTTTC 761
QY	467 ----- 467
Db	760 CAAGGACAGTCTCAACAGTGGCGCTGGGGCTCAATTGGTGGAGGAGGAGGTCGG 701
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Db	700 GCTCACCCCTCACAGGCTCCACTATCTCTGTAGCGCGCGTGGCTCCGCGCAGCTTGCT 641
QY	477 uLeuHisSerAlaAspGlyAlaGlyTyrgLuArgLeuValGlyAlaLeuAlaSerAlaLe 497
Db	640 CTTCACACTCGCGCAGCGAGCGGCTACGAGCGCTCTGGTGGAGCAGCTGGCGCTT 581
QY	497 uSerGlnMetProLeuArgValAlaValAspLeuTrpSerArgGluLeuSerAlaHi 517
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QY	517 sGlyAlaLeuAlaTrpPheHisGlnArgArgArgGileLeuGlnGluGlyValVa 537
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QY	577 eLeuGlnGlyArgAlaThrGlyArgTyrgValGlyValTyrgPheAspGlyLeuLeuHisPr 597
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QY	597 oAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGlnLeuPr 617
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Tue Aug 22 11:34:36 2006

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617 oAlaPheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAlaAspAr 637
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RESULT 8
LOCUS BG968034 784 bp mRNA linear EST 12-JUN-2001
DEFINITION 602832412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987035 5',
mRNA sequence.
ACCESSION BG968034
VERSION BG968034.1 GI:14355671
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 784)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10997 row: g column: 04
High quality sequence stop: 646.
FEATURES
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/db_xref="taxon:10090"
/clone="IMAGE:4987035"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP Co24"
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 6.76e-96 Length: 784
Score: 1187.00 Matches: 233
Percent Similarity: 89.7% Conservative: 3
Best Local Similarity: 88.6% Mismatches: 18
Query Match: 32.9% Indels: 10
DB: 2 Gaps: 2
US-10-719-202-2 (1-674) x BG968034 (1-784)

234 LeuAenHisThrAspLeuValProCysLeuCysIleGlnValTrpSerLeuGluProAsp 253
3 TTAACCCACAGACCTGTTCCCTGCTCTGCAATTCAGGTGTGTCGTAGAGCCAGAC 62
254 SerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsnLeuTrp 273
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274 HisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAspAlaProCysCys 293
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294 LeuProGlyLysValThrLeuCysTrpGlnAlaProAspGlnSerProCysGlnProLeu 313
183 CTCGCCGGCAGGTAACTGCTGCTGGCAGCCACAGACCCAGAGTCCCTGCCAGCCACTT 242
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543 CACCAGTGTATATGACAGCTGTGGACGATGACACATGGGATCGCTATGGGCTGCCCAT 602
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603 GGACAAAGTACATCCACAGCGCTGGTACTAGTATGGTGGCTGCTACTCTCTGGGCT 662
453 -----AlaAlaLeuPhePheLeuLeuLysLysAspArgArg-LysAlaAlaAa 470
663 GACGGCGCATTTATCATCTCGCTCCATCTTAAGAAAAGGACCCGAGGAAAGGGCCCG 722
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LOCUS BB609618 RIKEN full-length enriched, 18 days embryo Mus musculus
DEFINITION CDNA clone 1110025H02 5', mRNA sequence.
ACCESSION BB609618
VERSION BB609618.1 GI:16451334
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 1006)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
TITLE Yoshihide Hayashizaki
JOURNAL Unpublished (2001)
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic

```

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.

Location/Qualifiers

1. 1006

/organism="Mus musculus"

/mol_type="mRNA"

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/notes="Site 1: XhoI; Site 2: SstI; cDNA library was
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGCGCGCCCAACTCAGTGTGTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGAGTCCAGAGCTCAATTAAATTAATTAACCCCGCCCCC 3'].

cDNA was cleaved with XhoI and SstI."

Alignment Scores:

Pred. No.: 5,48e-92 Length: 1006

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Best Local Similarity: 70.1% Mismatches: 41

Query Match: 31.8% Indels: 55

DB: 7 Gaps: 7

US-10-719-202-2 (1-674) x BB609618 (1-1006)

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Db 74 GACCTGGTGCA-CCTGGTCACTCCGCTGCTTCTGCGGTATTGACTGTTTCGAGGCTAGT 132

Qy 163 LeuGlyAlaGluValGlnIleTrrpSerTyrrThrllysProArgTyrrGlnLysGluLeuAen 182

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Qy 183 LeuThrGlnGlnLeuPro----- 188

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Qy 218 uLysSerLeuTrrpTyrrLysAenLeuThrGlyProGlnAenIleThrLeuAenHisThrAs 238

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Qy 258 uPheCysProPheArgGluAspProGlyAlaHisArgAenLeuTrrpHisIleAlaArgLe 278

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Qy 278 uArgValLeuSerProGlyValTrrpGlnLeuAspAlaProCysCysLeuProGlyLysVa 298

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Db 613 AACACTGTGTGGCAGCGCCACAGCAGAGTCTCTGCGCCACTTGTGCCACAGTGC 672

Qy 318 oGlnLysAenAlaThrValAenGluProGlnAspPheGlnLeuValAlaGlyHisProAs 338

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Qy 378 snThrSerValCysAlaLeuGluProSerGly-CysThrProLeuProSerMetAlaSer 397

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Db 904 ACTGCTCGCTGGAGA-----GAGTTCCTGA--GACTTGCATAAACAT----- 943

Qy 418 GlnLeuTrrpAenAspAenMetGlySerLeuTrrpAlaCysProMetAspLysTyrrIle 437

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RESULT 10

AI007139

LOCUS

DEFINITION

AI007139

AI007139

AI007139

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[illegible]

Tue Aug 22 11:34:36 2006

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Db 329 GCCTGGCTCAGTGGCTGCTACCGATTCTCTGCAAGCCGGCGACCGGCCCTACGTC 270

Qy 588 GlyValTyrPheAspGlyLeuLeuHisProAspSerValProSerProPheArgValAla 607

Db 269 GGGGTCTACTTCCAGCGGCTCTGCACCCAGACTCTGTGCTCCCTCCCGTTCGGCTGCC 210

Qy 608 ProLeuPheSerLeuProThrGlnLeuProAlaPheLeuAspAlaLeuGlnGlyCys 627

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Qy 668 GlyProCysThrThrLeuGlu 674

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RESULT 13

CK474183

LOCUS

DEFINITION AGENCOURT 17619644 NIH_MGC_236 Rattus norvegicus cDNA clone

IMAGE:7129543 5', mRNA sequence.

ACCESSION CK474183.1 GI:40818281

VERSION Rattus norvegicus (Norway rat)

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Daniela S. Gerhard, Ph.D.

COMMENT Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-remail.nih.gov

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM15027 row: f column: 05

High quality sequence stop: 661.

Location/Qualifiers

1..739

/organism="Rattus norvegicus"

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/tissue_type="kidney, pooled"

/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_236"

/note="Organ: kidney; Vector: pExpress-1; Site: 1: EcorV;

Site: 2: NotI; RNA obtained from pooled kidney tissue from

a mix of male and female animals at 8 wk old. Tissues were

snap-frozen and kept at -80C for two days before RNA

extraction and purification (Tri-reagent method). cDNA was

primed using oligo-dT primer.

5'-pGACTAGTTCATGATCGAGCGCGCCGCC(7)25-3' and cloned into

the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_235) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores: 1.99e-83 Length: 739

Pred. No.: 1048.00 Matches: 190

Score: 85.2% Conservative: 17

Percent Similarity: 85.2% Mismatches: 36

Best Local Similarity: 78.2% Indels: 0

Query Match: 29.1% Gaps: 0

DB: 5

US-10-719-202-2 (1-674) x CK474183 (1-739)

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Db 121 ATTACTTTAAACCACTGACCTGGTTCCCTGCTCTGCATTCAGTTATGGTCTCAGGAG 180

Qy 252 ProAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaHisArgAsn 271

Db 181 CAGACTCTGTAGGACCACTTCTGCCCTTCAAGAAAGATCCCGTGCACACAGGAAC 240

Qy 272 LeuTrpHisIleAlaArgLeuArgValLeuSerProGlyValTyrGlnLeuAspAlaPro 291

Db 241 CTTTGGCACAATGGCCAGGCTGGGGTGCAGTCTCTCAGGAGCTGGCTGTAGACACGCT 300

Qy 292 CysCysLeuProGlyLysValThrLeuCysTyrGlnAlaProAspGlnSerProCysGln 311

Db 301 TGCTCTCTACGACCGAGGTGGCACTGTGTGGCGAGGACCAAGAGTCCCTGCTGCAG 360

Qy 312 ProLeuValProValProGlnLysAsnAlaThrValAsnGluProGlnAspPheGln 331

Db 361 CCCCTTGTGCCACCAATGCCCCAGAGAGTGTCACTATGAATAGGCCATTTAGTTCCCA 420

Qy 332 LeuValAlaGlyHisProAsnLeuCysValGlnValSerThrTyrGluLeuValGlnLeu 351

Db 421 TTGGTGAAGAAACACCCCAACCTCTGTCTCCAGGTGACGAGCTGGGAGAGGTTGAGTC 480

Qy 352 GlnAlaCysSerTyrAlaAspSerLeuGlyProPheLysAspAspMetLeuLeuValGlu 371

Db 481 CAAGAGTGTCTTGGGGTGACCTCTTAGGGCCCTTCAAGGATGATATGCTGTAGTGAG 540

Qy 372 MetLysThrGlyLysAsnAsnThrSerValCysAlaLeuGluProSerGlyCysThrPro 391

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RESULT 14

CK770217

LOCUS

DEFINITION 958358 MARC 1BOV Bos taurus cDNA 3', mRNA linear

EST 20-FEB-2004

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ACCESSION CK770217
VERSION CK770217.1 GI:42724311
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
        Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
        Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
        Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
        Quackenbush, J. and Keefe, J.W.
        1 (bases 1 to 884)
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
        libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called with phred v0.020425.c and
        trimmed with the aid of the trim_alt option. Vector identified with
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        Plater, 87 row: K column: 20
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                Library made from pooled tissue from lymph node, ovary,
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FEATURES
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        Library made from pooled tissue from lymph node, ovary,
        fat, hypothalamus, and pituitary."

ORIGIN
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Score: 1040.50 Matches: 191
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Best Local Similarity: 68.5% Mismatches: 59
Query Match: 28.9% Indels: 1
DB: 5 Gaps: 1

US-10-719-202-2 (1-674) x CK770217 (1-884)
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RESULT 15
BB625706/c
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DEFINITION Mus musculus cDNA clone 9330110N14 5', mRNA sequence.
ACCESSION BB625706
VERSION BB625706.1 GI:16463928
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 643)
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
        Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
        Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
        Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
        Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
        Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
        Takada, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
        RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
        Unpublished (2001)
        Contact: Yoshihide Hayashizaki
        Laboratory for Genome Exploration Research Group, RIKEN Genomic
        Sciences Center (GSC), Yokohama Institute
        The Institute of Physical and Chemical Research (RIKEN)
        1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
        Tel: 81-45-503-9222
        Fax: 81-45-503-9216
        Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
        Carninci, P., Shibata, Y., Hayata, N., Sugahara, Y., Shibata, K.,
        Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
        Normalization and subtraction of cap-trapper-selected cDNAs to
        prepare full-length cDNA libraries for rapid discovery of new
        genes. Genome Res. 10 (10), 1617-1630 (2000)
        wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
        Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

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Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
SOURCE

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Location/Qualifiers
1 643
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCTTTTGTTCCTTTTTTTTTTTTNN 3'], cDNA was
transcribed by using trihalonase thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 195.0. Second
strand cDNA was prepared with the primer adapted of
sequence [5' GAGAGAGAGATTCGATTATTAATATACCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda PUC 1. Cloning sites, 5' end: Sali; 3' end:
BamHI"

ORIGIN

Alignment Scores:	1.03e-82	643
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119-10-719-202-2 (1-674) x BB625706 (1-643)

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Qy	516	AlaHisGlyAlaLeuAlaTrpPheHisGlnArgArgGlnLeuGlnGluGlyGly	535
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536	ValValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnClnTrpLeuGlnLeu	555
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556	GlnThrValGluProGlyProHisAspAlaLeuAlaTrpLeuSerCysValLeuPro	575
403	CAGACAGTGGAGCCCGGGCGCGCATGACGCCCTCGCGCCTGGCTCAGCTTCGCTGCTACCC	344
576	AspPheLeuGlnGlyArgAlaThrGlyArgTyrValGlyValTyrPheAspGlyLeuLeu	595
343	GATTTCCTGCAAGGCCGGCGCACCGCGCGTACGTGGGTCTACTTCGACGGGCTGCTG	284
596	HisProAspSerValProSerProPheArgValAlaProLeuPheSerLeuProThrGln	615
283	CACCACGACTCTGTGCCCTCGCCCGTTCCGGGTGCGCCCGCTCTTCTCCCTGCCCTCGCAG	224
616	LeuProAlaPheLeuAspAlaLeuGlnGlyCysSerThrSerAlaGlyArgProAla	635
223	CTGCGGGCTTTCTCGATGCACTGACGAGGAGCTGCTCCACTTCGGCGGGCGACCGCG	164
636	AspArgValcIuargValThrGlnAlaLeuArgSerAlaLeuAspSerCysThrSerSer	655
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656	SerGluAlaProGlyCysCysGlnClnTrpPheLeuGlyProCysThrThrLeuGlu	674
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Search completed: August 17, 2006, 13:15:31
Job time : 6905 secs

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5	3572.5	99.1	683	6	US-11-150-533-26
6	3569.5	99.0	689	6	US-11-150-533-30
7	3565	98.9	698	3	US-09-863-818A-8
8	3565	98.9	698	4	US-10-749-144-8
9	3565	98.9	698	5	US-10-924-667-8
10	3562	98.8	698	3	US-09-866-050A-509
11	3539	98.2	698	4	US-10-416-442A-75
12	2352.5	65.3	692	3	US-09-899-471-8
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RESULT 2

US-10-719-202-2

; Sequence 2, Application US/10719202

; Publication No. US20040121388A1

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Murine Cytokine Receptor

; FILE REFERENCE: 00-46

; CURRENT APPLICATION NUMBER: US/10/719,202

; CURRENT FILING DATE: 2003-11-21

; PRIOR APPLICATION NUMBER: US/09/899,471

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 674

; TYPE: PRT

; ORGANISM: mouse

US-10-719-202-2

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Best Local Similarity 100.0%; Pred. No. 0;
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Qy 421 NDDNMGSLWACPMCKYIHRHWWLVWMLACLLAAALFFFLLLKKORRKAARGSRRTALLIHS 480
Db 421 NDDNMGSLWACPMCKYIHRHWWLVWMLACLLAAALFFFLLLKKORRKAARGSRRTALLIHS 480
Qy 481 ADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSSAHGALAWFHQRRRILOEGGVWILL 540
Db 481 ADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSSAHGALAWFHQRRRILOEGGVWILL 540
Qy 541 FSPAQAQCOQWLQLOTVPEPGPHDALAAWLSCVLPDFLOGRATGRYVGVYFDGLLHPDSV 600
Db 541 FSPAQAQCOQWLQLOTVPEPGPHDALAAWLSCVLPDFLOGRATGRYVGVYFDGLLHPDSV 600
Qy 601 PSPFRVAPLFLSLPTQLPAFLDALOGGCTSGRPAADRVERVTOALRSALDSCSSSEAPG 660
Db 601 PSPFRVAPLFLSLPTQLPAFLDALOGGCTSGRPAADRVERVTOALRSALDSCSSSEAPG 660
Qy 661 CCEWDLGPCTTLE 674
Db 661 CCEWDLGPCTTLE 674

RESULT 3
US-09-899-471-5
; Sequence 5, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 698
; TYPE: PRT
; ORGANISM: mouse
US-09-899-471-5

Query Match      99.4%; Score 3583; DB 3; Length 698;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

Qy 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQAPGPV 60
Db 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQAPGPV 60
Qy 61 LVPTRLOTELVRCPQKTDICALRVVVVHLAVHGHWAEPPEAGKSDSELOESRNASLQAO 120
Db 61 LVPTRLOTELVRCPQKTDICALRVVVVHLAVHGHWAEPPEAGKSDSELOESRNASLQAO 120
Qy 121 VVLSFOAYPIARCALLEVQVPADLVQPGOSVGSVAVDFDCEASLGAEVQIWSYTKPRYQKE 180
Db 121 VVLSFOAYPIARCALLEVQVPADLVQPGOSVGSVAVDFDCEASLGAEVQIWSYTKPRYQKE 180
Qy 181 LNLTLQPLDGDNVLLTLDSVEEQDFSLLYLRPVPDALKSLMYKNLTGPQNTILNHTDLV 240
Db 181 LNLTLQPLDGDNVLLTLDSVEEQDFSLLYLRPVPDALKSLMYKNLTGPQNTILNHTDLV 240
Qy 217 ALKSLWYKNTLQFQNTILNHTDLVPCLCIQVWSLEPDSERVECPFPREDPGAHNLWHIAR 276
Db 241 ALKSLWYKNTLQFQNTILNHTDLVPCLCIQVWSLEPDSERVECPFPREDPGAHNLWHIAR 300
Qy 277 RLRVLSPGVWQOLDAPCCLPCKVTLQWAPQSPQCPQLVPPVQKNAVTVNPFQDFQLVAGH 336
Db 301 RLRVLSPGVWQOLDAPCCLPCKVTLQWAPQSPQCPQLVPPVQKNAVTVNPFQDFQLVAGH 360
Qy 337 PNLVCQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALESFGCTPLPSMA 396
Db 361 PNLVCQVSTWEKVQLOACSWADSLGPFKDDMLLVEMKTGLNNTSVCALESFGCTPLPSMA 420
Qy 397 STRAARLGEELLQDFRSHQCMQLWDDNMGSLWACPMCKYIHRHWWLVWMLACLLAAALF 456
Db 397 STRAARLGEELLQDFRSHQCMQLWDDNMGSLWACPMCKYIHRHWWLVWMLACLLAAALF 456

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Db 421 STRAARLGEELLQDFRSHQCMQWLNDDNMGSLMACPMCKYIHRRWLVWVLACLLAALF 480
Qy 457 FFLLLKKDRKKAARGSTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
Db 481 FFLLLKKDRKKAARGSTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
Qy 517 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQWLQLOTVBPGPHDALAAMLSCVLPD 576
Db 541 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQWLQLOTVBPGPHDALAAMLSCVLPD 600
Qy 577 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLPSLTQLPAPLFDALOGGCSSTAGRPAD 636
Db 601 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLPSLTQLPAPLFDALOGGCSSTAGRPAD 660
Qy 637 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 674
Db 661 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 698

RESULT 4
US-10-719-202-5
; Sequence 5, Application US/10719202
; Publication No. US20040121388A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10/719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 698
; TYPE: PRT
; ORGANISM: mouse
US-10-719-202-5

Query Match 99.4%; Score 3583; DB 4; Length 698;
Best Local Similarity 96.6%; Pred.No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

Qy 1 MPVSWFLLSLALGRNPVWVSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Db 1 MPVSWFLLSLALGRNPVWVSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Qy 61 LVPTRLQTELVLRCPOKTDICALRVVHVLAHGHWAEPBEEAGKSDSELQESRNASLQAQ 120
Db 61 LVPTRLQTELVLRCPOKTDICALRVVHVLAHGHWAEPBEEAGKSDSELQESRNASLQAQ 120
Qy 121 VVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPRYQKE 180
Db 121 VVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPRYQKE 180
Qy 181 LNUITQQLP-----DGDVLLTLDVSEEDFSLYLRLRPVD 216
Db 181 LNUITQQLPDCRGLEVRDSIOSCWVLPWLVNSTDGDVLLTLDVSEEDFSLYLRLRPVD 240
Qy 217 ALKSLWYKNTLGPQNTLNHTDLVPCLCIQWMSLEPDSERVEFCPPREDPGAHRNLWHIA 276
Db 241 ALKSLWYKNTLGPQNTLNHTDLVPCLCIQWMSLEPDSERVEFCPPREDPGAHRNLWHIA 300
Qy 277 RLRVLSFGVWQOLDAPCCLPGKVTLCWQAPDQSPQPLVPVPPQKNATVNEPQDFQVAGH 336
Db 301 RLRVLSFGVWQOLDAPCCLPGKVTLCWQAPDQSPQPLVPVPPQKNATVNEPQDFQVAGH 360
Qy 337 PNLGVSTWKEVQLOACSWADSLGPPKDDMLLVEMKTLGNNTSVCALEPSSGCTPLPSMA 396
Db 361 PNLGVSTWKEVQLOACSWADSLGPPKDDMLLVEMKTLGNNTSVCALEPSSGCTPLPSMA 420
Qy 397 STRAARLGEELLQDFRSHQCMQWLNDDNMGSLMACPMCKYIHRRWLVWVLACLLAALF 456

Db 421 STRAARLGEELLQDFRSHQCMQWLNDDNMGSLMACPMCKYIHRRWLVWVLACLLAALF 480
Qy 457 FFLLLKKDRKKAARGSTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
Db 481 FFLLLKKDRKKAARGSTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
Qy 517 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQWLQLOTVBPGPHDALAAMLSCVLPD 576
Db 541 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQWLQLOTVBPGPHDALAAMLSCVLPD 600
Qy 577 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLPSLTQLPAPLFDALOGGCSSTAGRPAD 636
Db 601 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLPSLTQLPAPLFDALOGGCSSTAGRPAD 660
Qy 637 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 674
Db 661 RVERVTOALRSALDSCTSSSEAPGCCREWDLGPCTTLE 698

RESULT 5
US-11-150-533-26
; Sequence 26, Application US/11150533
; Publication No. US2006002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilsborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; FILE REFERENCE: 04-06P1
; CURRENT APPLICATION NUMBER: US/11/150,533
; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-150-533-26

Query Match 99.1%; Score 3572.5; DB 6; Length 683;
Best Local Similarity 98.2%; Pred.No. 0;
Matches 671; Conservative 1; Mismatches 2; Indels 9; Gaps 1;

Qy 1 MPVSWFLLSLALGRNPVWVSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Db 1 MPVSWFLLSLALGRNPVWVSLERLMBPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAPGV 60
Qy 61 LVPTRLQTELVLRCPOKTDICALRVVHVLAHGHWAEPBEEAGKSDSELQESRNASLQAQ 120
Db 61 LVPTRLQTELVLRCPOKTDICALRVVHVLAHGHWAEPBEEAGKSDSELQESRNASLQAQ 120
Qy 121 VVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPRYQKE 180
Db 121 VVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCPFEASIGAEVQIWSYTKPRYQKE 180
Qy 181 LNUITQQLP-----DGDVLLTLDVSEEDFSLYLRLRPVDALKSLWYKNTLGPON 231
Db 181 LNUITQQLPVLVPLVNSTDGDVLLTLDVSEEDFSLYLRLRPVDALKSLWYKNTLGPON 240
Qy 232 ITLNHTDLVPCLCIQWMSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSFGVWQOLDAP 291
Db 241 ITLNHTDLVPCLCIQWMSLEPDSERVEFCPPREDPGAHRNLWHIARLVLSFGVWQOLDAP 300
Qy 292 CCLPGKVTLCWQAPDQSPQPLVPVPPQKNATVNEPQDFQVAGHNLGVSTWKEVQLO 351
Db 301 CCLPGKVTLCWQAPDQSPQPLVPVPPQKNATVNEPQDFQVAGHNLGVSTWKEVQLO 360

QY	352	QACSWADSLGPKDDMLLVEMKTKGLNNTSVCALEPSCGCTPLPSPMASTRAARLGEELLQDF	411
Db	361	QACUWADSLGPKDDMLLVEMKTKGLNNTSVCALEPSCGCTPLPSPMASTRAARLGEELLQDF	420
QY	412	RSHOCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALFFFLKLLKDRRKAARG	471
Db	421	RSHOCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALFFFLKLLKDRRKAARG	480
QY	472	SRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFHHORRIL	531
Db	481	SRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFHHORRIL	540
QY	532	QEGGVWILLFSPAAVAOCQWLQOTVEPGPHDALAAWLSCVLPDFLQGRATGRVGVYF	591
Db	541	QEGGVWILLFSPAAVAOCQWLQOTVEPGPHDALAAWLSCVLPDFLQGRATGRVGVYF	600
QY	592	DGLLHPDSVPSPFRVAPLFSLPOLPAFLDALQGGCSTSAGRPADRVERVTOALRSALDS	651
Db	601	DGLLHPDSVPSPFRVAPLFSLPOLPAFLDALQGGCSTSAGRPADRVERVTOALRSALDS	660
QY	652	CTSSSEAPGCCCEWDLGPCTTLE	674
Db	661	CTSSSEAPGCCCEWDLGPCTTLE	683
RESULT 6			
US-11-150-533-30			
; Sequence 30, Application US/11150533			
; Publication No. US20060002925A1			
; GENERAL INFORMATION:			
; APPLICANT: Presnell, Scott R.			
; APPLICANT: Burkhead, Steven K.			
; APPLICANT: Levin, Steven D.			
; APPLICANT: Kuestner, Rolf E.			
; APPLICANT: Gao, Zeren			
; APPLICANT: Jaspers, Stephen R.			
; APPLICANT: Bilborough, Janine			
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14			
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN			
; TITLE OF INVENTION: INFLAMMATION			
; FILE REFERENCE: 04-06P1			
; CURRENT APPLICATION NUMBER: US/11/150,533			
; CURRENT FILING DATE: 2005-06-10			
; NUMBER OF SEQ ID NOS: 66			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 30			
; LENGTH: 689			
; TYPE: PRT			
; ORGANISM: Mus musculus			
US-11-150-533-30			
Query Match 99.0%; Score 3569.5; DB 6; Length 689;			
Best Local Similarity 97.4%; Pred. No. 0;			
Matches 671; Conservative 1; Mismatches 2; Indels 15; Gaps 1;			
QY	1	MPVSWFLLSIALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQSPGV	60
Db	1	MPVSWFLLSIALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQSPGV	60
QY	61	LVPTRLQTELVLRCPOKTDCALRVVRVHLAVHGHWAEPPEEAGKSDSELQESRNASLOAQ	120
Db	61	LVPTRLQTELVLRCPOKTDCALRVVRVHLAVHGHWAEPPEEAGKSDSELQESRNASLOAQ	120
QY	121	VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGAEVQIWSYTKPRYQKE	180
Db	121	VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGAEVQIWSYTKPRYQKE	180
QY	181	LNLTQQLP-----DGDNVLLTLDVSEEDQDFSLIYLRPVPD	225
Db	181	LNLTQQLPDCRGLVRSIQSCWDGDNVLLTLDVSEEDQDFSLIYLRPVPD	240
QY	226	LTGPQNTITLHNTDLVPCLCIQVWSLEPDSERVEFCPPREFDGAHRNLWHIARLVSPGV	285
us-10-719-202-2.rapbm			
Db	241	LTPQNTITLHNTDLVPCLCIQVWSLEPDSERVEFCPPREFDGAHRNLWHIARLVSPGV	300
QY	286	WQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKATVNEPQDFQIVAGHPNLCVQVST	345
Db	301	WQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKATVNEPQDFQIVAGHPNLCVQVST	360
QY	346	WEKVQIQAQSWADSLGPKDDMLLVEMKTKGLNNTSVCALEPSCGCTPLPSPMASTRAARLGE	405
Db	361	WEKVQIQAQSWADSLGPKDDMLLVEMKTKGLNNTSVCALEPSCGCTPLPSPMASTRAARLGE	420
QY	406	ELQDQFERSHOCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALFFFLKLLKDR	465
Db	421	ELQDQFERSHOCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALFFFLKLLKDR	480
QY	466	RKAARSRRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFHH	525
Db	481	RKAARSRRTALLHSADGAGYERLVGALASALSMPLRVAVDLWSRELSAHGALAWFHH	540
QY	526	ORRRILOEGGVWILLFSPAAVAOCQWLQOTVEPGPHDALAAWLSCVLPDFLQGRATGR	585
Db	541	ORRRILOEGGVWILLFSPAAVAOCQWLQOTVEPGPHDALAAWLSCVLPDFLQGRATGR	600
QY	586	YGVYFVFDGLLHPDSVPSPFRVAPLFSLPOLPAFLDALQGGCSTSAGRPADRVERVTOAL	645
Db	601	YGVYFVFDGLLHPDSVPSPFRVAPLFSLPOLPAFLDALQGGCSTSAGRPADRVERVTOAL	660
QY	646	RSALDSCSSSEAPGCCCEWDLGPCTTLE	674
Db	661	RSALDSCSSSEAPGCCCEWDLGPCTTLE	689
RESULT 7			
US-09-863-818A-8			
; Sequence 8, Application US/09863818A			
; Publication No. US20030092881A1			
; GENERAL INFORMATION:			
; APPLICANT: Gorman, Daniel M.			
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS			
; FILE REFERENCE: DX01170K			
; CURRENT APPLICATION NUMBER: US/09/863,818A			
; CURRENT FILING DATE: 2001-05-23			
; PRIOR APPLICATION NUMBER: US 60/206,862			
; PRIOR FILING DATE: 2000-05-24			
; NUMBER OF SEQ ID NOS: 22			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 8			
; LENGTH: 698			
; TYPE: PRT			
; ORGANISM: Mus musculus			
US-09-863-818A-8			
Query Match 98.9%; Score 3565; DB 3; Length 698;			
Best Local Similarity 96.1%; Pred. No. 0;			
Matches 671; Conservative 1; Mismatches 2; Indels 24; Gaps 1;			
QY	1	MPVSWFLLSIALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQSPGV	60
Db	1	MPVSWFLLSIALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQSPGV	60
QY	61	LVPTRLQTELVLRCPOKTDCALRVVRVHLAVHGHWAEPPEEAGKSDSELQESRNASLOAQ	120
Db	61	LVPTRLQTELVLRCPOKTDCALRVVRVHLAVHGHWAEPPEEAGKSDSELQESRNASLOAQ	120
QY	121	VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGAEVQIWSYTKPRYQKE	180
Db	121	VVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCFEASIGAEVQIWSYTKPRYQKE	180
QY	181	LNLTQQLP-----DGDNVLLTLDVSEEDQDFSLIYLRPVPD	216
Db	181	LNLTQQLPDCRGLVRSIQSCWDGDNVLLTLDVSEEDQDFSLIYLRPVPD	240
QY	217	ALKSLWYKNTLTGPQNTITLHNTDLVPCLCIQVWSLEPDSERVEFCPPREFDGAHRNLWHIAT	276


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QY 217 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGARNLWHIA 276
DB 241 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGARNLWHIA 300
QY 277 RLRVLSPGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNATVNEPQDQLVAGH 336
DB 301 RLRVLSPGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNATVNEPQDQLVAGH 360
QY 337 PNLGVQVSTWKEVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPDSCTPLPSMA 396
DB 361 PNLGVQVSTWKEVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPDSCTPLPSMA 420
QY 397 STRAARLGEELLQDPRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 456
DB 421 STRAARLGEELLQDPRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 480
QY 457 FFLLLKKDORRKAARGSTRALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
DB 481 FFLLLKKDORRKAARGSTRALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
QY 517 HGALAWFHQRRIILOEGGVWILLFSPAQAACQOWLOLQTVPGPHDALAAWLSCVLPD 576
DB 541 HGALAWFHQRRIILOEGGVWILLFSPAQAACQOWLOLQTVPGPHDALAAWLSCVLPD 600
QY 577 FLOGRATGRYGVYFDGLLHPDSVSPRFRVAPFLFSLPTQLPAFLDALQGGCSTSAGRPAD 636
DB 601 FLOGRATGRYGVYFDGLLHPDSVSPRFRVAPFLFSLPTQLPAFLDALQGGCSTSAGRPAD 660
QY 637 RVERVTOALRSALDSTSSSEAPGCCCEWDLGPCTTLE 674
DB 661 RVERVTOALRSALDSTSSSEAPGCCCEWDLGPCTTLE 698

RESULT 10
US-09-866-050A-509
; Sequence 509, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 509
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-509

Query Match 98.8%; Score 3562; DB 3; Length 698;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 670; Conservative 2; Mismatches 2; Indels 24; Gaps 1;

QY 1 MPVSWFLLSLALGRNPVWVSLERLMEPQDPTARCSGLSCHLWDGDLVCLFGSLQSPGPV 60
DB 1 MPVSWFLLSLALGRNPVWVSLERLMEPQDPTARCSGLSCHLWDGDLVCLFGSLQSPGPV 60
QY 61 LVPTRQLTELVLRCPOKTDALCVRVVHVAHGHWAEPPEACKSSELSQESRNASLQAO 120
DB 61 LVPTRQLTELVLRCPOKTDALCVRVVHVAHGHWAEPPEACKSSELSQESRNASLQAO 120
QY 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSGVSAVDFCDCEASLGAEVQIWSYTKPRYQKE 180
DB 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSGVSAVDFCDCEASLGAEVQIWSYTKPRYQKE 180
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QY 181 LNTLTOQLP-----DGDNVLLTLDVSEEDQSFLLYLRPVDP 216
DB 181 LNTLTOQLPDCRGLEVRDSIQSCWVLPWLVSTDGDNVLLTLDVSEEDQSFLLYLRPVDP 240
QY 217 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGARNLWHIA 276
DB 241 ALKSLWYKNTGPNITLNHTDLVPCLCIQWSLEPDSERVEFCPPFRDPGARNLWHIA 300
QY 277 RLRVLSPGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNATVNEPQDQLVAGH 336
DB 301 RLRVLSPGVWQDAPCCLPKGVTLWCQAPDQSPQPLVPPVPQKNATVNEPQDQLVAGH 360
QY 337 PNLGVQVSTWKEVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPDSCTPLPSMA 396
DB 361 PNLGVQVSTWKEVQLQACSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPDSCTPLPSMA 420
QY 397 STRAARLGEELLQDPRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 456
DB 421 STRAARLGEELLQDPRSHQCMQWMDNMGSLWACPMCKYIHRRWLVWLAACLLAAALF 480
QY 457 FFLLLKKDORRKAARGSTRALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
DB 481 FFLLLKKDORRKAARGSTRALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
QY 517 HGALAWFHQRRIILOEGGVWILLFSPAQAACQOWLOLQTVPGPHDALAAWLSCVLPD 576
DB 541 HGALAWFHQRRIILOEGGVWILLFSPAQAACQOWLOLQTVPGPHDALAAWLSCVLPD 600
QY 577 FLOGRATGRYGVYFDGLLHPDSVSPRFRVAPFLFSLPTQLPAFLDALQGGCSTSAGRPAD 636
DB 601 FLOGRATGRYGVYFDGLLHPDSVSPRFRVAPFLFSLPTQLPAFLDALQGGCSTSAGRPAD 660
QY 637 RVERVTOALRSALDSTSSSEAPGCCCEWDLGPCTTLE 674
DB 661 RVERVTOALRSALDSTSSSEAPGCCCEWDLGPCTTLE 698

RESULT 11
US-10-416-442A-75
; Sequence 75, Application US/10416442A
; Publication No. US20040171109A1
; GENERAL INFORMATION:
; APPLICANT: Haudenschild, Dominik
; APPLICANT: Rose, Larry
; APPLICANT: Moseley, Timothy
; APPLICANT: Reddi, A. Hari
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: IL-17 Receptor-Like Protein, Uses Thereof, and
; TITLE OF INVENTION: Modulation of Catabolic Activity of IL-17 Cytokines on
; TITLE OF INVENTION: Bone and Cartilage
; FILE REFERENCE: 023070-115511US
; CURRENT APPLICATION NUMBER: US/10/416,442A
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/247,134
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/271,197
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/328,904
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: WO PCT/US01/43855
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse IL-17RL
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(698)
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OTHER INFORMATION: Xaa = any amino acid
US-10-416-442A-75

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Query Match      98.2%; Score 3539; DB 4; Length 698;
Best Local Similarity 95.4%; Pred. No. 9.3e-318;
Matches 666; Conservative 1; Mismatches 7; Indels 24; Gaps 1;

QY 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDLCLPGSLQSAAGPV 60
DB 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDLCLPGSLQSAAGPV 60

QY 61 LVPTRLOTELVLRCPOKTDALRVVVHLAVHGHWAEPPEAGKSDSELOESRNASLOAQ 120
DB 61 LVPTRLOTELVLRCPOKTDALRVVVHLAVHGHWAEPPEAGKSDSELOESRNASLOAQ 120

QY 121 VLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFASLGAEVQIWSYTKPYOKE 180
DB 121 VLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFASLGAEVQIWSYTKPYOKE 180

QY 181 LNTTQQLP-----DGDNVLLTLDVSEEQDFSLFLYLRVPD 216
DB 181 LNTTQQLPDCRGLEVRDSIQSCWVLPWLVNSTDGDNVLLTLDVSEEQDFSLFLYLRVPD 240

QY 217 ALKSLWYKNTLGTQNTLNTDLPCLCIQVWSLEPDSERVEPCPFREDPGAHRNLWHIA 276
DB 241 ALKSLWYKNTLGTQNTLNTDLPCLCIQVWSLEPDSERVEPCPFREDPGAHRNLWHIA 300

QY 277 RLRLVSPGVWQLDAPCLPGKVTLCQWAPDQSPCQPLVPPVPOKNATVNEPQDQFQVAGH 336
DB 301 RLRLVSPGVWQLDAPCLPGKVTLCQWAPDQSPCQPLVPPVPOKNATVNEPQDQFQVAGH 360

QY 337 PNLGVSTWKEVQLOACSWADSLGPKDMLLVEMKTLGNTSVCALEPSGCTPLPSMA 396
DB 361 PNLGVSTWKEVQLOACSWADSLGPKDMLLVEMKTLGNTSVCALEPSGCTPLPSMA 420

QY 397 STRAARLGBELLQDFRSHQCHQWLNDDNMGSLWACPMCKYIHRRWLVWLACILLAAALP 456
DB 421 STRAARLGBELLQDFRSHQCHQWLNDDNMGSLWACPMCKYIHRRWLVWLACILLAAALP 480

QY 457 FPLLLKKDRKKAARGSTRALLHSADGAGYERLVGALASALSQMLRVAVDLWSRRELSA 516
DB 481 FPLLLKKDRKKAARGSTRALLHSADGAGYERLVGALASALSQMLRVAVDLWSRRELSA 540

QY 517 HGALAWFHRRRILOEGGVVILLFSPAQAQCOQWLQQTVPFPHDAAWLSCVLPD 576
DB 541 HGALAWFHRRRILOEGGVVILLFSPAQAQCOQWLQQTVPFPHDAAWLSCVLPD 600

QY 577 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLFSLTQLPAPFLDALQGGCSTSAGRPAD 636
DB 601 FLOGRATGRVGVYFDGLLHPDSVPSFRVAPLFSLTQLPAPFLDALQGGCSTSAGRPAD 660

QY 637 RVERVTQALRSALDSCTSSSEAPGCCCEWDLGPTTLE 674
DB 661 RVERVTQALRSALDSCTSSSEAPGCCCEWDLGPTTLE 698

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RESULT 12
US-09-899-471-8
; Sequence 8, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Human
US-09-899-471-8

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Query Match      65.3%; Score 2352.5; DB 3; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDLCLPGSLQSAAGPV 60
DB 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDLCLPGSLQSAAGPV 60

QY 61 LVPTRLOTELVLRCPOKTDALRVVVHLAVHGHWAEPPEAGKSDSELOESRNAS 116
DB 61 LVPTRLOTELVLRCPOKTDALRVVVHLAVHGHWAEPPEAGKSDSELOESRNAS 120

QY 117 LQAVVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFASLGAEVQIWSYTKPR 176
DB 121 LQAVVLSFQAYPIARCALLLEVQPADLVQPGQSGVSAVDFCPFASLGAEVQIWSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSLFLYLRVPDALKWYKNTL 227
DB 181 YQKELNLTQQLPALPWLNVNSADGDNVHLVNLVSEEQHFLGSLYMNQVQGPCKPRHKNLT 240

QY 228 GPONITLNTDLPCLCIQVWSLEPDSERVEPCPFREDPGAHRNLWHIARLVLSPGVQ 287
DB 241 GPONITLNTDLPCLCIQVWSLEPDSERVEPCPFREDPGAHRNLWHIARLVLSPGVQ 300

QY 288 LQAPCCPLPGKVTLCQWAPDQSPCQPLVPPVPOKNATVNEPQDQFQVAGHNLVCVQVSTWE 347
DB 301 LQAPCCPLPAEALCWAPGDDFCQPLVPPVPSWENVTVDKLVLEFLLKGHENLVCVQVNSSE 360

QY 348 KVQLQACSWADSLGPKDMLLVEMKTLGNTSVCALEPSGCTPLPSMASTRARLGEEL 407
DB 361 KLQLOQCLWADSLGLPKDVLLETRGPQDNRSCLALEPSGCTSLPSKASTRAARLGEYL 420

QY 408 LQDFRSHQCHQWLNDDNMGSLWACPMCKYIHRRWLVWLACILLAAALPFLILLKKDRK 467
DB 421 LQDLOGGQCLQLW--DDLGALWACPMCKYIHRRWLVWLACILLAAALPFLILLKKDHAK 479

QY 468 AARGSTRALLHSADGAGYERLVGALASALSQMLRVAVDLWSRRELISAHGALAWFHHR 527
DB 480 AARGSTRALLHSADGAGYERLVGALASALSQMLRVAVDLWSRRELISAHGALAWFHHR 539

QY 528 RLRLVSPGVWQLDAPCLPGKVTLCQWAPDQSPCQPLVPPVPOKNATVNEPQDQFQVAGH 584
DB 540 RLRLVSPGVWQLDAPCLPGKVTLCQWAPDQSPCQPLVPPVPOKNATVNEPQDQFQVAGH 599

QY 585 RYGVYFDGLLHPDSVPSFRVAPLFSLTQLPAPFLDALQGGCSTSAGRPADRVERVTOA 644
DB 600 SYVGACDFRLLHPDAVPALFRTVVPFTLPSQLPFLDALQGGCSTSAGRPADRVERVTOA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LQPALDSYFHPGTPAPG 677

RESULT 13
US-10-458-647-2
; Sequence 2, Application US/10458647
; Publication No. US20030199041A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Pownder, Sarah L.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-50
; CURRENT APPLICATION NUMBER: US/10/458,647
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US/09/608,918
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 692
; TYPE: PRT

```

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; ORGANISM: Homo sapiens
US-10-458-647-2

Query Match      65.3%; Score 2352.5; DB 4; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLSLALGRNPVVSLERLMEPQDTCALRVVVHLAVHGHWAEPBEE-----AGKSDSELOESRNAS 116
DB 1 MPVSWFLSLALGRSPVLSLERLVGPQDATHCPSGLSCLRWSDSILCLPGDIVPAQGPV 60

QY 61 LVPRLQTELVLRCQKTCDCALRVVVHLAVHGHWAEPBEE-----AGKSDSELOESRNAS 116
DB 61 LAPHQLTELVLRCQKTCDCALRVVVHLAVHGHWAEPBEEDEEKFAGGAADSGVPEPRNAS 120

QY 117 LQAQVVLFSQAYPIARCALLEVQPADLVQPGQSVGSAVDFCFEASLGAEQVINSYTKPR 176
DB 121 LQAQVVLFSQAYPIARCALLEVQPADLVQPGQSVGSAVDFCFEASLGAEQVINSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSLLYLPVPDALKSLWYKNLT 227
DB 181 YQKELNLTQQLPALPWLNVNSADGDNVHLVNVSEHQFGLSLYWNQVQGPCKPRWHKNLT 240

QY 228 GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCFPREDPGAHRLNWHIARLVLSPGVWQ 287
DB 241 GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCFPREDPGAHRLNWHIARLVLSPGVWQ 300

QY 288 LDAPCCLPGKVTLCWQADPQSCQPLVPPVPOKNAVNEPQDFQLVAGHPNLCVQVSTWE 347
DB 301 LDAPCCLPAEALCWRAAPGDCQPLVPPVPSWENVTVDKLEFPLLLKGHPLNCVQVNSE 360

QY 348 KYVQLQACSWADSLGPKDMLVEMKTLGNNTSVCALEPSGCTPLPSMASTAAALGEBEL 407
DB 361 KIQLECLWADSLGPKDMLVEMKTLGNNTSVCALEPSGCTPLPSMASTAAALGEBEL 420

QY 408 LQDFRSHQCMQVNDNNGSLWACPMCKYIHRRWVWLACLLAAALFFFLLLKKDRRK 467
DB 421 LQDLQSGCQLQLW-DDDLGALWACPMCKYIHRRWVWLACLLAAALFFFLLLKKDRRK 479

QY 468 AARGSTALLHSADGAGYERLVGALASALSQMLRVAVDLWSRRELSAHGALAWFHQR 527
DB 480 AARGRAALLYSADDSGFERLVGALASALSQMLRVAVDLWSRRELSAHGALAWFHQR 539

QY 528 RRILEGVWVLLFSPAQAACQWMLQOTVEP---GPHDALAAWLSVLPDFLQGRATG 584
DB 540 RQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGAGHPHDAFRASLSVLPDFLQGRAPG 599

QY 585 RYGVYFDGLLHSDVSPSRVAPLPSLTQPLPAFLDALQGGCSTSGAGPADRVERTQA 644
DB 600 SYVGACFDRLLHPDAVPALFRTVFTLPSQLPDLFGLAQQPAPRSGRLQERAEQVSRA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LQPALDSYFHPGTPAPG 677

RESULT 14
US-10-719-202-8
; Sequence 8, Application US/10719202
; Publication No. US2004012138A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/10719,202
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/899,471
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 692
; TYPE: PRT

; ORGANISM: Human
US-10-719-202-8

Query Match      65.3%; Score 2352.5; DB 4; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLSLALGRNPVVSLERLMEPQDTCALRVVVHLAVHGHWAEPBEE-----AGKSDSELOESRNAS 116
DB 1 MPVSWFLSLALGRSPVLSLERLVGPQDATHCPSGLSCLRWSDSILCLPGDIVPAQGPV 60

QY 61 LVPRLQTELVLRCQKTCDCALRVVVHLAVHGHWAEPBEE-----AGKSDSELOESRNAS 116
DB 61 LAPHQLTELVLRCQKTCDCALRVVVHLAVHGHWAEPBEEDEEKFAGGAADSGVPEPRNAS 120

QY 117 LQAQVVLFSQAYPIARCALLEVQPADLVQPGQSVGSAVDFCFEASLGAEQVINSYTKPR 176
DB 121 LQAQVVLFSQAYPIARCALLEVQPADLVQPGQSVGSAVDFCFEASLGAEQVINSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEQDFSLLYLPVPDALKSLWYKNLT 227
DB 181 YQKELNLTQQLPALPWLNVNSADGDNVHLVNVSEHQFGLSLYWNQVQGPCKPRWHKNLT 240

QY 228 GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCFPREDPGAHRLNWHIARLVLSPGVWQ 287
DB 241 GPQNTILNHTDLVPCLCIQVMSLEPDSERVEFCFPREDPGAHRLNWHIARLVLSPGVWQ 300

QY 288 LDAPCCLPGKVTLCWQADPQSCQPLVPPVPOKNAVNEPQDFQLVAGHPNLCVQVSTWE 347
DB 301 LDAPCCLPAEALCWRAAPGDCQPLVPPVPSWENVTVDKLEFPLLLKGHPLNCVQVNSE 360

QY 348 KYVQLQACSWADSLGPKDMLVEMKTLGNNTSVCALEPSGCTPLPSMASTAAALGEBEL 407
DB 361 KIQLECLWADSLGPKDMLVEMKTLGNNTSVCALEPSGCTPLPSMASTAAALGEBEL 420

QY 408 LQDFRSHQCMQVNDNNGSLWACPMCKYIHRRWVWLACLLAAALFFFLLLKKDRRK 467
DB 421 LQDLQSGCQLQLW-DDDLGALWACPMCKYIHRRWVWLACLLAAALFFFLLLKKDRRK 479

QY 468 AARGSTALLHSADGAGYERLVGALASALSQMLRVAVDLWSRRELSAHGALAWFHQR 527
DB 480 AARGRAALLYSADDSGFERLVGALASALSQMLRVAVDLWSRRELSAHGALAWFHQR 539

QY 528 RRILEGVWVLLFSPAQAACQWMLQOTVEP---GPHDALAAWLSVLPDFLQGRATG 584
DB 540 RQTLQEGGVVLLFSPGAVALCSEWLQDGVSGGAGHPHDAFRASLSVLPDFLQGRAPG 599

QY 585 RYGVYFDGLLHSDVSPSRVAPLPSLTQPLPAFLDALQGGCSTSGAGPADRVERTQA 644
DB 600 SYVGACFDRLLHPDAVPALFRTVFTLPSQLPDLFGLAQQPAPRSGRLQERAEQVSRA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LQPALDSYFHPGTPAPG 677

RESULT 15
US-11-150-533-2
; Sequence 2, Application US/11150533
; Publication No. US20060002925A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Burkhead, Steven K.
; APPLICANT: Levin, Steven D.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bilsborough, Janine
; TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-06PI
; CURRENT APPLICATION NUMBER: US/11/150,533

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; CURRENT FILING DATE: 2005-06-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-150-533-2

Query Match      65.3%; Score 2352.5; DB 6; Length 692;
Best Local Similarity 67.4%; Pred. No. 6e-208;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

Qy 1 MPVSWFLSLALGRNPVVVSLERLMEPDQARCSGLSLCHLWDGDLVLCPLGSLQSAFGPV 60
Db 1 MPVPMFLSLALGRSPVVLRLVGPQDATHCSPLGSLCRLMDSDLICLPDGVPAFGPV 60

Qy 61 LVPTRLQTELVLRCPOKTDLCALRVVVVHLAVHGHWAEPBE----AKSDSELOESRNAS 116
Db 61 LAPTHLQTELVLRCQKETDCDLRLVAVHLAVHGHMEEPDEEKFGGADSGVEEPRNAS 120

Qy 117 LQAGVLSFOAYPTARCALLEVOVPADLVQPGQSVGSAVDCPEASIGAEVQIMSYTKPR 176
Db 121 LQAGVLSFOAYPTARCALLEVOVPADLVQPGQSVGVVYDCFEAALGSEVRIMSYTQPR 180

Qy 177 YQKELNLTQQLP-----DGNVLLTLVDSEEQDFSLLYLRPVDPDALKSLWYKNLT 227
Db 181 YKELNHTQQLPALPMLNVSDAGDNVHLVNVSEQHFGLSLYWNQVQGPCKPRHKNLT 240

Qy 228 GPQNTILNHTDLVPCLCIQWLSLEPDSERVEFCPFREDPCAHNRLWHIARLVLSGVWQ 287
Db 241 GPQIITLNTDLVPCLCIQWPLEPDSVRTNICPFREDPRAHQNLWQAARLLTLQSWL 300

Qy 288 LDAPCCLPGKVTLCQAPQDOSCPQPLVPPVQKNATVNEPQDQOLVAGHNLGVQVSTWE 347
Db 301 LDAPCSLFABAALCWAPGDPQCPQLVPLPSWENVTVDKVLEPPLKGGHNLGVQVNSSE 360

Qy 348 KVQLQACSWADSLGPPKDDMLLVEMTKGLNNTSVCALEPSGCTPLPSMASTRAARLGEEL 407
Db 361 KLQLQECNLWADSLGPLKDDVLLLETRGPQDNRSICALPSGCTSLPSKASTRAARLGEYL 420

Qy 408 LQDFRSHQCQMLNNDNMGSLMACPMQKXIHRRWLVWLACLALLAAALFFFLLLKKDRRK 467
Db 421 LQDLQSGQCILQW-DDDLGALMACPMQKXIHKRWLVWLACLFPAAALSLLILLKKDHAK 479

Qy 468 AARGSRFALLHSDAGCYERLVGALASALQMPRLRVAVDLWSRRELSAHGALANWFHQH 527
Db 480 AAARGRAALLLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVAFHAQR 539

Qy 528 RRILQEGGVILLFSPAAVAQCOQWLQQTVER---GPHDALAAWLSCVLPDFLQGRATG 584
Db 540 RQTLQEGGVVILLFSPGAVALCSEWLQDQVSGPGAGHGFHDAFRASLSCVLPDFLQGRAPG 599

Qy 585 RYVGVPDGLLHPDSVSPFRVAPLFSLSPTQLPAFLDALQGGCSTAGRPADRVETQA 644
Db 600 SYVGACFDRLHDPDAVPALEFVFTVFTLPSQLPDFLQALQOPRAPRSGRLEQERAEQVSR 659

Qy 645 LRSALDSC--TSSSEAPG 660
Db 660 LQPALDSYFHPGPGTAPG 677
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Search completed: August 16, 2006, 11:51:00
Job time : 182 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2006, 11:37:07 ; Search time 199 Seconds
(without alignments)

1548.562 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

Sequence: 1 MPVSWFLSLALGRNPVVVS.....SSEAPGCCCEWDLGPCTTLE 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

9: Geneseq2005s:*

10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3605	100.0	674	5 AAE14559	AAE14559 Murine cy
2	3583	99.4	698	5 AAE14560	AAE14560 Murine cy
3	3572.5	99.1	683	10 AEF05373	Aef05373 Mouse zcy
4	3569.5	99.0	689	10 AEF05377	Aef05377 Mouse zcy
5	3565	98.9	698	5 AAU11354	AAU11354 Mouse DNA
6	3565	98.9	698	9 AEB55652	Aeb55652 Mouse DCS
7	3562	98.8	698	5 ABB72297	Abb72297 Murine pr
8	3539	98.2	698	5 AAU93161	AAU93161 Mouse int
9	2352.5	65.3	692	4 AAB61880	Aab61880 Human cyt
10	2352.5	65.3	692	5 AAE14562	AAE14562 Human cyt
11	2352.5	65.3	692	7 ABW01911	ABw01911 Human cyt
12	2352.5	65.3	692	10 AEF05349	Aef05349 Human IL1
13	2348.5	65.1	449	10 AEF05374	Aef05374 Mouse zcy
14	2339	64.9	705	4 AAB61884	Aab61884 Chimeric
15	2339	64.9	705	4 AAU29322	AAU29322 Human PRO
16	2339	64.9	705	4 AAB87606	Aab87606 Human PRO
17	2339	64.9	705	4 AAU04956	AAU04956 Human Int
18	2339	64.9	705	5 ABG95931	Abg95931 Human sec
19	2339	64.9	705	5 ABB84998	Abb84998 Human PRO
20	2339	64.9	705	5 ABB95604	Abb95604 Human PRO
21	2339	64.9	705	6 ABU58698	Abu58698 Human ang
22	2339	64.9	705	6 ABU88246	Abu88246 Novel hum
23	2339	64.9	705	6 ABU84561	Abu84561 Human sec

ABr66435 Human sec
ABr65825 Human sec
ABu99765 Human sec
ABu83004 Human PRO
ABu90125 Novel hum
ABr68374 Human sec
ABu96427 Novel hum
ABu92858 Human sec
ABO08935 Human sec
ABO02987 Human sec
ABr75141 Human sec
ABr94903 Human sec
ABu85876 Human PRO
ABu99036 Novel hum
ABu98251 Novel hum
ABu91957 Novel hum
ABu89650 Human PRO
ABu8491 Human sec
ABu67704 Human sec
ABu80732 Human PRO
ABu90956 Novel hum
ABr99650 Human sec

ALIGNMENTS

RESULT 1

AAE14559
ID AAE14559 standard; protein; 674 AA.

XX
AC AAE14559;

XX
DT 17-MAY-2002 (first entry)

XX
DB Murine cytokine receptor, Zcytor14.

XX
KW Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;

KW gene therapy; protein therapy; receptor.

XX
OS Mus sp.

XX
FH Key

FT Peptide

FT Protein

FT Domain

FT Domain

FT Domain

FT Domain

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arthritis, and as educational tools or in research.

Claim 1; Page 90-91; 99pp; English.

The present sequence is murine cytokine receptor, Zcytor14. The Zcytor14 polypeptide is useful for identifying or isolating Zcytor14 ligands, in preparing antibodies, in identifying proteins or peptide cleavage sites, in amino acid sequence analysis, and in monitoring biological activities of both the native and tagged protein in vitro or in vivo. Polypeptides having Zcytor14 activity can be used to treat inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational tool in genetics, molecular biology, protein chemistry and antibody production analysis, in the preparation of expression constructs for bacterial, viral or mammalian expression, in determining mRNA and DNA localisation of Zcytor14 polynucleotide in tissues, for identifying related polynucleotides and polypeptides by nucleic acid hybridisation, in linkage-based testing for various diseases in murine models, and to determine whether a subject's chromosomes contain a mutation in the Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo diagnosis, and for detecting and localising Zcytor14 gene expression in tissue samples

Sequence 674 AA;

Query Match 100.0%; Score 3605; DB 5; Length 674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCIPGSLQAPGPV 60
1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCIPGSLQAPGPV 60

61 LVPTRQTELVLCRCPKTDLCALRVVVHLAVGHWAEPPEEAGKSDSELQESRNASLQQA 120
61 LVPTRQTELVLCRCPKTDLCALRVVVHLAVGHWAEPPEEAGKSDSELQESRNASLQQA 120

121 VLSFQAYPIARCALLEVQPADLVPGQSVGSVAVDFCFEASIGAEVQVWSYTKRYQKE 180
121 VLSFQAYPIARCALLEVQPADLVPGQSVGSVAVDFCFEASIGAEVQVWSYTKRYQKE 180

181 LNTQQLPDGDNVLLTLDVSEEDFSLVLRVPDALKSLWYKNTLGPQNTLNTHTDLV 240
181 LNTQQLPDGDNVLLTLDVSEEDFSLVLRVPDALKSLWYKNTLGPQNTLNTHTDLV 240

241 PCLCIQVWSLEPDSERVEFCFPREDPGAHNLMHIALRLVLSPGVQLDAPCCLPGKVTI 300
241 PCLCIQVWSLEPDSERVEFCFPREDPGAHNLMHIALRLVLSPGVQLDAPCCLPGKVTI 300

301 CWQAPDQSPQPLVPPVPQKNATNEPQDFQVAGHPNLCVQVSTWEKVQLQACSWADSL 360
301 CWQAPDQSPQPLVPPVPQKNATNEPQDFQVAGHPNLCVQVSTWEKVQLQACSWADSL 360

361 GPFKDDMLLVEMTKGLNNTSVCALEPSGCTPLPSMASTRALRGEELLQDFRSHQCWLW 420
361 GPFKDDMLLVEMTKGLNNTSVCALEPSGCTPLPSMASTRALRGEELLQDFRSHQCWLW 420

421 NDDNMGSLWACPMQDIYHRRVWVWLACLLAALFFLLIKDORRKAAGSRATLLHS 480
421 NDDNMGSLWACPMQDIYHRRVWVWLACLLAALFFLLIKDORRKAAGSRATLLHS 480

481 ADGAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHQRRLIQEGGVILL 540
481 ADGAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHQRRLIQEGGVILL 540

541 FSPAFAVACQWQLQVTEPGPHDAAWLSVLPDFLQGRATGRYGVVFDGLLHDPDV 600
541 FSPAFAVACQWQLQVTEPGPHDAAWLSVLPDFLQGRATGRYGVVFDGLLHDPDV 600

601 PSPFRVAFVLSPTQLPAFLDALQGGCSTAGRPADRVVTVQALRSALDCTSSSEAPG 660
601 PSPFRVAFVLSPTQLPAFLDALQGGCSTAGRPADRVVTVQALRSALDCTSSSEAPG 660

661 CCEEWDLGPCTTLE 674

661 CCEEWDLGPCTTLE 674

RESULT 2

AAE14560 standard; protein; 698 AA.

AAE14560;

17-MAY-2002 (first entry)

Marine cytokine receptor Zcytor14 variant, Zcytor14-1.

Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;

gene therapy; protein therapy; Zcytor14-1; receptor.

Mus sp.

Location/Qualifiers

21..464

/label= Extracellular domain

/note= "Specifically claimed"

WO200204519-A2.

17-JAN-2002.

05-JUL-2001; 2001WO-US021344.

06-JUL-2000; 2000US-0216446P.

(ZYMO) ZYMOGENETICS INC.

Gao Z;

WPI; 2002-179701/23.

N-PSDB; AAD24222.

New murine cytokine receptor, Zcytor14, and polynucleotides encoding the

receptor, useful for treating inflammation, specifically rheumatoid

arthritis, and as educational tools or in research.

Claim 1; Page 95-97; 99pp; English.

The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14

polypeptide is useful for identifying or isolating Zcytor14 ligands, in

preparing antibodies, in identifying proteins or peptide cleavage sites,

in amino acid sequence analysis, and in monitoring biological activities

of both the native and tagged protein in vitro or in vivo. Polypeptides

having Zcytor14 activity can be used to treat inflammation, such as

rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational

tool in genetics, molecular biology, protein chemistry and antibody

production analysis, in the preparation of expression constructs for

bacterial, viral or mammalian expression, in determining mRNA and DNA

localisation of Zcytor14 polynucleotide in tissues, for identifying

related polynucleotides and polypeptides by nucleic acid hybridisation,

in linkage-based testing for various diseases in murine models, and to

determine whether a subject's chromosomes contain a mutation in the

Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo

diagnosis, and for detecting and localising Zcytor14 gene expression in

tissue samples. The present sequence is murine Zcytor14 variant, Zcytor14

-1

Sequence 698 AA;

Query Match 99.4%; Score 3583; DB 5; Length 698;

Best Local Similarity 96.6%; Pred. No. 0;

Matches 674; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCIPGSLQAPGPV 60
1 MPVSWFLLSALGRNPVVVSLERLMEPQDTARCSIGLSCHLWDGVDVLCIPGSLQAPGPV 60

QY 61 LVPTRLQTELVLRCPOKTDCAIRVVRVHVAHGHMAEPBEAGKSDSELOESRNASLQAA 120
 DB 61 LVPTRLQTELVLRCPOKTDCAIRVVRVHVAHGHMAEPBEAGKSDSELOESRNASLQAA 120
 QY 121 VLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCFEASLGAEVQIWSYTKPRYQKE 180
 DB 121 VLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCFEASLGAEVQIWSYTKPRYQKE 180
 QY 181 LNLQTOQLP-----DGNVLLTLDVSEEDFSLLYLRVPVD 216
 DB 181 LNLQTOQLPDCGLEVRDSIQSCWVLPWLVNSTGDGNVLLTLDVSEEDFSLLYLRVPVD 240
 QY 217 ALKSLWYKNLTGPNITLHTDLVPCLCIQWSLEPDSERVEFCPPREDPCAHNRLWHIA 276
 DB 241 ALKSLWYKNLTGPNITLHTDLVPCLCIQWSLEPDSERVEFCPPREDPCAHNRLWHIA 300
 QY 277 RLRLVSGVWQDAPCCLPGKVTYLCWAQPDQSPQCPPLVPPVQKNATVNEPQDPQLVAGH 336
 DB 301 RLRLVSGVWQDAPCCLPGKVTYLCWAQPDQSPQCPPLVPPVQKNATVNEPQDPQLVAGH 360
 QY 337 PNLCCVQVSTWEKVQLOACSWADSLGPKDDMLLVEMKTLGNTSVCALEPSGCTPLPSMA 396
 DB 361 PNLCCVQVSTWEKVQLOACSWADSLGPKDDMLLVEMKTLGNTSVCALEPSGCTPLPSMA 420
 QY 397 STRAARLGEELLQDFRSHQCHQWLNDDNMGSLWACPMDKYTHRRWLVWLACLLAAALF 456
 DB 421 STRAARLGEELLQDFRSHQCHQWLNDDNMGSLWACPMDKYTHRRWLVWLACLLAAALF 480
 QY 457 PFLLLKXDRKAARGSTRALLHSGADGAGYERLVGALASALSQMLPRAVDLMSRRBSA 516
 DB 481 PFLLLKXDRKAARGSTRALLHSGADGAGYERLVGALASALSQMLPRAVDLMSRRBSA 540
 QY 517 HGAIAWPHORRRILQSGGVVILLFSPAQAQCOOVLQOTVEPGRHDAALWLSCVLPD 576
 DB 541 HGAIAWPHORRRILQSGGVVILLFSPAQAQCOOVLQOTVEPGRHDAALWLSCVLPD 600
 QY 577 FLOGRATGRVGVYDFGLLHPDSVPSFRVAPLPSLTQLPAPFADALQGGCSTISAGRPA 636
 DB 601 FLOGRATGRVGVYDFGLLHPDSVPSFRVAPLPSLTQLPAPFADALQGGCSTISAGRPA 660
 QY 637 RVERVTQALRSALDSTSSSEAPGCCBEWDLGPTTILE 674
 DB 661 RVERVTQALRSALDSTSSSEAPGCCBEWDLGPTTILE 698

RESULT 3

ABF05373

ID ABF05373 standard; protein; 683 AA.

XX AC

XX AC

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10-JUN-2005; 2005WO-US020521.

10-JUN-2004; 2004US-0578805P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;

Jaspers SR, Billsborough J;

WPI; 2006-067457/07.

N-PSDB; ABF05372.

New isolated soluble receptor comprises at least one Zcytor14 subunit,

useful for treating an inflammatory disease, e.g. asthma, inflammatory

bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or

psoriasis.

Disclosure; SEQ ID NO 26; 205pp; English.

The invention describes an isolated soluble receptor comprises at least

one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide

comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises

amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ

ID NO. 24) given in the specification. Also described are: an isolated

soluble receptor comprising Zcytor14, where Zcytor14 comprises a

polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces

the pro-inflammatory activity of either IL-17A comprising fully defined 153

amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153

amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds

to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),

and where the antibody or antibody fragment reduces the pro-inflammatory

activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);

reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal

afflicted with an inflammatory disease in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

role; and treating a pathological condition in which IL-17A or IL-17F plays a

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role; and treating a pathological condition in which IL-17A or IL-17F plays a

Query Match 99.1%; Score 3572.5; DB 10; Length 683;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 671; Conservative 1; Mismatches 2; Indels 9; Gaps 1;

QY 1 MPVSWFLLSLALGRNPVWVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAGPV 60
 DB 1 MPVSWFLLSLALGRNPVWVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQSAAGPV 60
 QY 61 LVPTRLQTELVLRCPOKTDCAIRVVRVHVAHGHMAEPBEAGKSDSELOESRNASLQAA 120
 DB 61 LVPTRLQTELVLRCPOKTDCAIRVVRVHVAHGHMAEPBEAGKSDSELOESRNASLQAA 120
 QY 121 VLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCFEASLGAEVQIWSYTKPRYQKE 180
 DB 121 VLSFQAYPIARCALLEVQVPADLVQPGQSVGSVAVDFCFEASLGAEVQIWSYTKPRYQKE 180
 QY 181 LNLQTOQLP-----DGNVLLTLDVSEEDFSLLYLRVPVDKSLWYKNLTGPN 231
 DB 181 LNLQTOQLPFWLVNSTGDGNVLLTLDVSEEDFSLLYLRVPVDKSLWYKNLTGPN 240
 QY 232 ITLNLHTDLVPCLCIQWSLEPDSERVEFCPPREDPCAHNRLWHIARLRLVLSFGVWQDAP 291
 DB 241 ITLNLHTDLVPCLCIQWSLEPDSERVEFCPPREDPCAHNRLWHIARLRLVLSFGVWQDAP 300
 QY 292 CCLPGKVTILCWQAPDQSPQCPPLVPPVQKNATVNEPQDPQLVAGHNPCLVQVSTWTKVQL 351
 DB 301 CCLPGKVTILCWQAPDQSPQCPPLVPPVQKNATVNEPQDPQLVAGHNPCLVQVSTWTKVQL 360

QY 646 RSALDCTSSSEAPGCCCEWDLGPCTTLE 674
 DB 661 RSALDCTSSSEAPGCCCEWDLGPCTTLE 689

RESULT 5
 AAU11354
 ID AAU11354 standard; protein; 698 AA.
 AC AAU11354;
 XX
 DT 26-MAR-2002 (first entry)
 DE Mouse DNAX cytokine receptor subunit 7 (DCRS7) polypeptide.
 XX
 KW Mouse; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling;
 KW gene therapy; protein therapy; immunological disorder.
 OS Mus musculus.
 XX
 FN WO200190358-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016767.
 XX
 PR 24-MAY-2000; 2000US-0206862P.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Gorman DM;
 XX
 DR WPI; 2002-106198/14.
 DR N-PSDB; AAS18132.
 XX
 PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
 PT useful for detecting antibodies generated in response to presence of
 PT increased protein levels or immunological disorders.
 XX
 PS Disclosure; Page 20; 148pp; English.
 XX
 CC The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents the mouse DCRS7 polypeptide
 XX
 SQ Sequence 698 AA;

Query Match 98.9%; Score 3565; DB 5; Length 698;
 Best Local Similarity 96.1%; Pred. No. 0;
 Matches 671; Conservative 1; Mismatches 2; Indels 24; Gaps 1;

QY 1 MPVSWFLSLALGRNPVVVSLERLMEPDQTARCSLGLSCHLWDGVDVLCPLGSLQAPGV 60
 DB 1 MPVSWFLSLALGRNPVVVSLERLMEPDQTARCSLGLSCHLWDGVDVLCPLGSLQAPGV 60
 QY 61 LVPTLQTLVLCRCQKTDTCALRVVVVHLVGHWAEPKGSDELQSRNASLQ 120
 DB 61 LVPTLQTLVLCRCQKTDTCALRVVVVHLVGHWAEPKGSDELQSRNASLQ 120
 QY 121 VVLSFQAYPIARCALLEVQVPADLVQPGQVGSVAFDCFEASLGAEVQIWSYTKRYOKE 180
 DB 121 VVLSFQAYPIARCALLEVQVPADLVQPGQVGSVAFDCFEASLGAEVQIWSYTKRYOKE 180

QY 181 LNLTTQQLP-----DGDNVLLTLDVSEEDQDFSLLYLRPVPD 216
 DB 181 LNLTTQQLPDCRCGLEVRDSIQCWVLPWLVNSTDGDNVLLTLDVSEEDQDFSLLYLRPVPD 240
 QY 217 ALKSLWYKNLTGPQNTITLNTHTDLVPCLCIQWSLEPDSERVEFCFPFREDPGAHNLMHIA 276
 DB 241 ALKSLWYKNLTGPQNTITLNTHTDLVPCLCIQWSLEPDSERVEFCFPFREDPGAHNLMHIA 300
 QY 277 RLRVLSPGVWQLDAPCCCLPGKVTLCWQAPDQSPQPLVPVPOKNATVNBPDQDLVAGH 336
 DB 301 RLRVLSPGVWQLDAPCCCLPGKVTLCWQAPDQSPQPLVPVPOKNATVNBPDQDLVAGH 360
 QY 337 PNLGVQVSTWVKVQLQACSWADSLGPKDDMLLVEMKTLNNTSVCALEPFGCTPLFSMA 396
 DB 361 PNLGVQVSTWVKVQLQACSWADSLGPKDDMLLVEMKTLNNTSVCALEPFGCTPLFSMA 420
 QY 397 STAAARLGBELLQDFSHQCMQWLNDDNMGSLWACPMCKYIHRRWLVWVLAALLAAALF 456
 DB 421 STAAARLGBELLQDFSHQCMQWLNDDNMGSLWACPMCKYIHRRWLVWVLAALLAAALF 480
 QY 457 FFLLLKKDRKKAARGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLMSRRLESA 516
 DB 481 FFLLLKKDRKKAARGSRRTALLHSADGAGYERLVGALASALSOMPLRVAVDLMSRRLESA 540
 QY 517 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQMLQQTVEPDPHDALAAALSCVLPD 576
 DB 541 HGALAWFHQRRILOEGGVVILLFSPAQAQCOQMLQQTVEPDPHDALAAALSCVLPD 600
 QY 577 FLQGRATGRYGVYFDGLLHPDSVPSFRVAPLFSLPQTQLPAFLDALQGCSTSAGRPAD 636
 DB 601 FLQGRATGRYGVYFDGLLHPDSVPSFRVAPLFSLPQTQLPAFLDALQGCSTSAGRPAD 660
 QY 637 RVERVTOALRSALDCTSSSEAPGCCCEWDLGPCTTLE 674
 DB 661 RVERVTOALRSALDCTSSSEAPGCCCEWDLGPCTTLE 698

RESULT 6
 AEB55652
 ID AEB55652 standard; protein; 698 AA.
 XX
 AC AEB55652;
 XX
 DT 22-SEP-2005 (first entry)
 DE Mouse DCSR7 polypeptide.
 XX
 KW Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
 KW DCSR; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
 KW interstitial lung disorder; asthma; allergy; atherosclerosis;
 KW gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
 KW antipsoriatic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
 KW antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
 KW IL-17C agonist; mouse; DCSR7; receptor; antisense therapy; RNAi therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20 /note= "signal peptide"
 FT Protein 21..698 /note= "mature protein"
 XX
 PN WO2005065711-A2.
 XX
 PD 21-JUL-2005.
 XX
 PF 22-DEC-2004; 2004WO-US042935.
 XX
 PR 29-DEC-2003; 2003US-00749144.
 XX
 PA (SCHE) SCHERING CORP.
 XX

PI Gorman DM;
XX WPI; 2005-506792/51.
DR N-PSDB; ABB55651.
XX
PT Modulating activity of cell, involves contacting cell with an agonist or
PT antagonist of DNAX cytokine receptor subunit.
XX
PS Example 5; SEQ ID NO 8; 130pp; English.
XX
XX The invention relates to modulating (M1) activity of cell, by contacting
CC cell with an agonist or antagonist of DNAX cytokine receptor subunit
CC (DCRS9) or of interleukin (IL)-17C where the cell modulates psoriasis,
CC inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
CC allergy, or atherosclerosis. Also provided are methods for treating (M2)
CC the disorders which involves administration of the modulator and
CC diagnosing (M3) a disorder as mentioned above that involves contacting a
CC sample from a test subject with a binding composition that specifically
CC binds to a polypeptide or nucleic acid of DCRS9 or IL-17C. (M1) is useful
CC for modulating an activity of a cell. (M2) is useful for treating a
CC subject suffering from a disorder such as psoriasis, IBD, interstitial
CC lung disorder, asthma or allergy, or atherosclerosis, where the
CC interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic
CC granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or
CC ulcerative colitis. The present sequence represents a mouse DCRS6
CC polypeptide.
XX
SQ Sequence 698 AA;

Query Match 98.9%; Score 3565; DB 9; Length 698;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 671; Conservative 1; Mismatches 2; Indels 24; Gaps 1;

QY 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVCLPGSLQAPGPV 60
DB 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVCLPGSLQAPGPV 60
QY 61 LVPTRLOTELVLRCQKTDALRVVVHVLVHGHWAEPPEAKGSDSELQESRNASLQAO 120
DB 61 LVPTRLOTELVLRCQKTDALRVVVHVLVHGHWAEPPEAKGSDSELQESRNASLQAO 120
QY 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSVGSAVDFCEASLGAEVQIWSYTKRYQKE 180
DB 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSVGSAVDFCEASLGAEVQIWSYTKRYQKE 180
QY 181 LNLTOQLP-----DGNVLLTLDVSEEDQFSLLYLRPVPD 216
DB 181 LNLTOQLPDCRGLEVRDSTQSCWVLPWLVNVTGDGNVLLTLDVSEEDQFSLLYLRPVPD 240
QY 217 ALKSLWYKMLTGQNTLNLHTDLVPCLCIQVWSLEPDSRVFCPPREDPGAHRLMWHIA 276
DB 241 ALKSLWYKMLTGQNTLNLHTDLVPCLCIQVWSLEPDSRVFCPPREDPGAHRLMWHIA 300
QY 277 RLRLVSPGVWLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVQKNATVNEPQDFOLVAGH 336
DB 301 RLRLVSPGVWLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVQKNATVNEPQDFOLVAGH 360
QY 337 PNLGVQVSTWVKVQLQACSWADSLGPFKDDMLLVEMKTLGNLNTSVCALEPFGCTPLPSMA 396
DB 361 PNLGVQVSTWVKVQLQACSWADSLGPFKDDMLLVEMKTLGNLNTSVCALEPFGCTPLPSMA 420
QY 397 STRAARLGBELLQDFRSHQCMQWLNDDNMGSLWACPMCKYIHRVWLVWLACLLIAALF 456
DB 421 STRAARLGBELLQDFRSHQCMQWLNDDNMGSLWACPMCKYIHRVWLVWLACLLIAALF 480
QY 457 FFLKKDKRRKARGRTALLHSAAGVYERLVGALASALSQMPURVAVDLWSRRELSA 516
DB 481 FFLKKDKRRKARGRTALLHSAAGVYERLVGALASALSQMPURVAVDLWSRRELSA 540
QY 517 HGAIAWFHRRILQEGGVVILLFSPAAVQACQWQLQOTVPEPGHDAALAWLSVCLPDP 576
DB 541 HGAIAWFHRRILQEGGVVILLFSPAAVQACQWQLQOTVPEPGHDAALAWLSVCLPDP 600

QY 577 FLOGRATGRVYGVYFDGLLHPDSSVPSRVPAPLPSLTQLPALFDALQGGCSTAGRPAD 636
DB 601 FLOGRATGRVYGVYFDGLLHPDSSVPSRVPAPLPSLTQLPALFDALQGGCSTAGRPAD 660
QY 637 RVERVTQALRSALDSCSTSSSEAPGCCBWDGLGPCCTTLE 674
DB 661 RVERVTQALRSALDSCSTSSSEAPGCCBWDGLGPCCTTLE 698
RESULT 7
ABB72297
ID ABB72297 standard; protein; 698 AA.
AC ABB72297;
XX
DT 04-APR-2002 (first entry)
XX Murine protein isolated from skin cells SEQ ID NO: 509.
DE Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
XX developmental defect; inflammatory disease; dermatological; vulnary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
KW
OS Mus sp.
XX WO200190357-A1.
XX
XX 29-NOV-2001.
XX 24-MAY-2001; 2001WO-NZ000099.
XX
XX 24-MAY-2000; 2000US-0206650P.
PR 25-JUL-2000; 2000US-0221232P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG;
PI Kumble KD;
XX
XX WPI; 2002-122020/16.
XX
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses.
XX
XX Claim 4; Page 314-315; 466pp; English.
XX
XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC polypeptide of the invention
XX
SQ Sequence 698 AA;

Query Match 98.8%; Score 3562; DB 5; Length 698;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 670; Conservative 2; Mismatches 2; Indels 24; Gaps 1;

QY 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVCLPGSLQAPGPV 60
DB 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVCLPGSLQAPGPV 60
QY 61 LVPTRLOTELVLRCQKTDALRVVVHVLVHGHWAEPPEAKGSDSELQESRNASLQAO 120
DB 61 LVPTRLOTELVLRCQKTDALRVVVHVLVHGHWAEPPEAKGSDSELQESRNASLQAO 120
QY 121 VVLSFOAYPIARCALLEVQVPADLVQPGQSVGSAVDFCEASLGAEVQIWSYTKRYQKE 180

Db 121 VVLSFOAYPIARCALLEVQPADLVQPGSGVSAVDFCFEASIGASVQIWSYTKPRYQKE 180
QY 181 LNLTTQQLP-----DGNVLLTLDVSEBQDFSELLYLTPVDP 216
Db 181 LNLTTQQLPDCRGLEVRDSTQSCWVLPWLVNSTDGDNVLLTLDVSEBQDFSELLYLTPVDP 240
QY 217 ALKSLWYKXLTGPQNTLNHTDLVPLCLCQVMSLEPDSERVEFCPPRPDPGAGRNLWHIA 276
Db 241 ALKSLWYKXLTGPQNTLNHTDLVPLCLCQVMSLEPDSERVEFCPPRPDPGAGRNLWHIA 300
QY 277 RLRLVSPGWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVQKNATVNEPQDFQLVAGH 336
Db 301 RLRLVSPGWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVQKNATVNEPQDFQLVAGH 360
QY 337 PNLGVQVSTWVKVQLQACSWASLSGPKDDMLLVEMKTLGNNTSVCALESPSGCTPLPSNA 396
Db 361 PNLGVQVSTWVKVQLQACSWASLSGPKDDMLLVEMKTLGNNTSVCALESPSGCTPLPSNA 420
QY 397 STRAARLGBELLQDFRSHQCMQLWNNDDNMGSLWACPMCKYIHRWVWLVMLACILLAAALF 456
Db 421 STRAARLGBELLQDFRSHQCMQLWNNDDNMGSLWACPMCKYIHRWVWLVMLACILLAAALF 480
QY 457 PFLLLKXDRKKAARGSRRTALLHSADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSA 516
Db 481 PFLLLKXDRKKAARGSRRTALLHSADGAGYERLVGALASALSQMPRLRVAVDLWSRRELSA 540
QY 517 HGAALWFHQRRIILQEGGVWILLFSPAQAQOQWLQOTVEPGHDAALAWLSVLPD 576
Db 541 HGAALWFHQRRIILQEGGVWILLFSPAQAQOQWLQOTVEPGHDAALAWLSVLPD 600
QY 577 FLQGRATGRYGVYFDGLLHPDSVSPFRVAPLPSLPTQLPAFLDALQGCSTSAGRPAD 636
Db 601 FLQGRATGRYGVYFDGLLHPDSVSPFRVAPLPSLPTQLPAFLDALQGCSTSAGRPAD 660
QY 637 RVERVTQALRSALDSCSTSEAPGCCEWDLGPTTLE 674
Db 661 RVERVTQALRSALDSCSTSEAPGCCEWDLGPTTLE 698

RESULT 8
AAU99161
ID AAU99161 standard; protein; 698 AA.
AC AAU99161;
XX
DT 24-SEP-2002 (first entry)
XX
DE Mouse Interleukin 17 receptor like protein, IL-17RL.
KW Mouse; receptor; Interleukin 17 receptor-like protein; IL-17RL;
KW Chondrooleukin; bone degradation; cartilage degradation; gene therapy;
KW chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW allergic skin immune response; organ transplant rejection; cytokine;
KW osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
KW seronegative spondyloarthropathy; bone morphogenetic protein.
XX
OS Mus sp.
XX

Key Location/Qualifiers
FH Key /label= UNKNOWN
FT Misc-difference 627 /note= "Encoded by CSS"
FT Misc-difference 655 /label= UNKNOWN
FT /note= "Encoded by SCG"
FT Misc-difference 668 /label= UNKNOWN
FT /note= "Encoded by SCC"
FT Misc-difference 682 /label= UNKNOWN
FT /note= "Encoded by SCC"
XX

PN WO200238764-A2.
XX 16-MAY-2002.
XX 13-NOV-2001; 2001WO-US043855.
XX 10-NOV-2000; 2000US-0247134P.
PR 23-FEB-2001; 2001US-0271137P.
PR 12-OCT-2001; 2001US-0328904P.
XX (REGC) UNIV CALIFORNIA.
XX Haudenschild D, Rose L, Moseley T, Reddi AH;
PI WPI; 2002-508211/54.
XX N-PSDB; ABR6568.
DR Interleukin-17 receptor-like polypeptide useful for the manufacture of a
XX medicament to modulate cartilage or bone growth in a mammal.
XX Claim 83; Page 89-90; 108pp; English.
XX The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC polypeptide, with 85% or greater sequence identity to a polypeptide with
CC a sequence appearing as AAU98781-AAU98792, where IL-17RL binds to an IL-
CC 17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F. Also included
CC are IL-17RL polynucleotides, antibodies, expression cassettes, transgenic
CC host cells, a method of determining the aggressiveness of a prostate
CC cancer cell, by determining the presence or absence in the cell of a
CC group of IL-17RL (where the determination that the group is absent in the
CC cell indicates that the cancer is more aggressive than a like cell in
CC which the group is present) and a mammalian cell comprising a
CC polynucleotide encoding an IL-17B antagonist, where the cell is selected
CC from chondrocyte, synovocyte, and mesenchymal stem cell. IL-17RL or the
CC polynucleotide is useful for the manufacture of a medicament to modulate
CC cartilage or bone growth in a mammal. The polynucleotide is useful for
CC the manufacture of a medicament to restore androgen-responsiveness to a
CC prostate cancer cell. IL-17RL is useful for decreasing catabolic activity
CC in bone or cartilage in a mammal. IL-17RL is useful for inhibiting
CC ossification or calcification in a mammal suffering from pathological
CC ossification or calcification, for diagnosing a cartilage degenerative
CC disorder in a mammal, for inhibiting the rate of proteoglycan synthesis
CC by a chondrocyte in culture, and for the manufacture of a medicament to
CC potentiate the activity of a bone morphogenetic protein in a mammal. An
CC IL-17RL antagonist is useful for treating a bone or cartilage pathology
CC such as a degenerative cartilage disorder selected from osteoarthritis,
CC rheumatoid arthritis, relapsing polychondritis, seronegative
CC spondyloarthropathies, multiple sclerosis, allergic skin immune response
CC and organ transplant rejection. IL-17RL is particularly a receptor for IL
CC -17B (Chondrooleukin, a proinflammatory cytokine). The gene for IL-17RL is
CC located on chromosome 3p25.3-3p24.1. The present sequence is the full
CC length sequence for mouse IL-17RL
XX Sequence 698 AA;
SQ

Query Match 98.2%; Score 3539; DB 5; Length 698;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 666; Conservative 1; Mismatches 7; Indels 24; Gaps 1;
QY 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSGLSGLHWDGVDVLCPLGSLQSPGPV 60
Db 1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSGLSGLHWDGVDVLCPLGSLQSPGPV 60
QY 61 LVPTRLQTELVLRCPOKTDLCALRVVVHVLAVGHWAEPBEAGKSDSELSERNASLQAO 120
Db 61 LVPTRLQTELVLRCPOKTDLCALRVVVHVLAVGHWAEPBEAGKSDSELSERNASLQAO 120
QY 121 VVLSFOAYPIARCALLEVQPADLVQPGSGVSAVDFCFEASIGASVQIWSYTKPRYQKE 180
Db 121 VVLSFOAYPIARCALLEVQPADLVQPGSGVSAVDFCFEASIGASVQIWSYTKPRYQKE 180
QY 181 LNLTTQQLP-----DGNVLLTLDVSEBQDFSELLYLTPVDP 216

Db 181 LNLTLQQLPDCRGLEVRDSIQSCWVLPWLVNSTDGNVLLTLVDSEEQDFSLYLRLRPVD 240
Qy 217 ALKSLWYKXNLGPQNITLNLHTDLVPCLCIQWNSLEPDSERVEFCPPFRDPGAHRLMWHIA 276
Db 241 ALKSLWYKXNLGPQNITLNLHTDLVPCLCIQWNSLEPDSERVEFCPPFRDPGAHRLMWHIA 300
Qy 277 RLRLVSPGVQWLDAPCCLPKGVTLQWAPDQSPQPLVPPVPQKNATVNEPQDFOLVAGH 336
Db 301 RLRLVSPGVQWLDAPCCLPKGVTLQWAPDQSPQPLVPPVPQKNATVNEPQDFOLVAGH 360
Qy 337 PNLVQVSTWEKVLQACSWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMA 396
Db 361 PNLVQVSTWEKVLQACSWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMA 420
Qy 397 STRAARLGEELLQDFRSHQWOLMNDNNGSLWACPMKXIHRRLVWLACLLLAALF 456
Db 421 STRAARLGEELLQDFRSHQWOLMNDNNGSLWACPMKXIHRRLVWLACLLLAALF 480
Qy 457 FFLLLKKDRLKAAGSRRTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 516
Db 481 FFLLLKKDRLKAAGSRRTALLLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSA 540
Qy 517 HGALAWFHQRRLILQEGGVILLFSPAQAQCCQWLQQTVEPGPHDALAAWLSCVLPD 576
Db 541 HGALAWFHQRRLILQEGGVILLFSPAQAQCCQWLQQTVEPGPHDALAAWLSCVLPD 600
Qy 577 FLOGRATGRYGVYDGLLHPSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPA 636
Db 601 FLOGRATGRYGVYDGLLHPSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPA 660
Qy 637 RVERVTQALRSALDSCSTSSSEAPGCCSEWDLGPCTTLE 674
Db 661 RVERVTQALRSALDSCSTSSSEAPGCCSEWDLGPCTTLE 698

RESULT 9

AAB61880
ID AAB61880 standard; protein; 692 AA.
XX AC AAB61880;
XX DT 08-MAY-2001 (first entry)
XX DE Human cytokine receptor Zcytor14.
XX KW Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
XX KW antiinflammatory; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO200104304-A1.
XX PD 18-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018383.
XX PR 07-JUL-1999; 99US-00348854.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Preanell SR, Burkhead SK, Powder SL;
XX WPI; 2001-112618/12.
XX DR N-PSDB; AAC85027.
XX PT New polypeptide encoding a human cytokine receptor Zcytor14, for treating
XX PT inflammation e.g. rheumatoid arthritis.
XX PS Claim 2; Page 2; 112pp; English.
XX CC The invention provides a new human cytokine receptor designated Zcytor14.
XX CC Zcytor14 can be expressed by standard recombinant methodology. The
XX CC encoding nucleic acid is useful for detecting the expression of a

CC Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC used to screen biological samples in vitro for the presence of Zcytor14.
CC Proteins, polypeptides and peptides having Zcytor14 activity can be
CC administered to a subject who lacks an adequate amount of this
CC polypeptide, for treating inflammation and conditions such as rheumatoid
CC arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC antibodies) can be used to treat a subject who produces an excess of
CC Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC Zcytor14 to a subject. The present sequence represents the human cytokine
CC receptor Zcytor14
XX
SQ Sequence 692 AA;
Query Match 65.3%; Score 2352.5; DB 4; Length 692;
Best Local Similarity 67.4%; Pred. No. 2e-216;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;
Qy 1 MPVSWFLLSLALGNRPVVVSLERLMEPQDARTCSLGLSCHLWDGVLCPLGSLQAPGV 60
Db 1 MPVSWFLLSLALGNRPVVVSLERLMEPQDARTCSLGLSCHLWDGVLCPLGSLQAPGV 60
Qy 61 LVPTRLQTELVLRCPOKTDCLALRVVVVHLAVHGHWAEP-AGKSDSLSQSRNAS 116
Db 61 LAPTHLQTELVLRCPOKTDCLALRVVVVHLAVHGHWAEP-AGKSDSLSQSRNAS 120
Qy 117 LQAOVVLFSQAVPIARCALLEVQVPADLVQPCQSVGSVAVFDCFEASLGAEOVWYTKPR 176
Db 121 LQAOVVLFSQAVPIARCALLEVQVPADLVQPCQSVGSVAVFDCFEASLGAEOVWYTKPR 180
Qy 177 YQKELNLTQQLP-----DGDNVLTLDVSEBQDFSLLYLRPVPDALKSLWYKNT 227
Db 181 YQKELNLTQQLP-----DGDNVLTLDVSEBQDFSLLYLRPVPDALKSLWYKNT 240
Qy 228 GPONITLNTHTDLVPCLCIQWNSLEPDSERVEFCPPFRDPGAHRLMWHIA 287
Db 241 GPONITLNTHTDLVPCLCIQWNSLEPDSERVEFCPPFRDPGAHRLMWHIA 300
Qy 288 LDAPCCLPGKVTLCWQAPDQSPQPLVPPVPOKNTAVNEPQDFQLVAGHPNLCVOVSTWE 347
Db 301 LDAPCCLPGKVTLCWQAPDQSPQPLVPPVPOKNTAVNEPQDFQLVAGHPNLCVOVSTWE 360
Qy 348 KVQLQACSWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMASTAAARLGEEL 407
Db 361 KLQLQACSWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSCGCTPLPSMASTAAARLGEEL 420
Qy 408 LQDFRSHQWOLMNDNNGSLWACPMKXIHRRLVWLACLLLAALFFLLKKDRK 467
Db 421 LQDFRSHQWOLMNDNNGSLWACPMKXIHRRLVWLACLLLAALFFLLKKDRK 479
Qy 468 AARGSRRTALLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAMPHQR 527
Db 480 AARGSRRTALLHSDAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALAMPHQR 539
Qy 528 RRILQEGGVILLFSPAQAQCCQWLQQTVEP---GPHDALAAWLSCVLPDFLOGRATG 584
Db 540 RRILQEGGVILLFSPAQAQCCQWLQQTVEP---GPHDALAAWLSCVLPDFLOGRATG 599
Qy 585 RVVGVYFDGLHPSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPA 644
Db 600 RVVGVYFDGLHPSVSPFRVAPLPSLTQLPALFDALOGGSGTSAGRPA 659
Qy 645 LRSALDSC--TSSEAPG 660
Db 660 LRSALDSC--TSSEAPG 677
RESULT 10
AAB14562
ID AAB14562 standard; protein; 692 AA.
XX AC AAB14562;
XX DT 17-MAY-2002 (first entry)

XX	Human cytokine receptor Zcytor14.	
DE	Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;	
XX	gene therapy; protein therapy; human; receptor.	
KW	Homo sapiens.	
XX	WO200204519-A2.	
XX	17-JAN-2002.	
XX	05-JUL-2001; 2001WO-US021344.	
PF	06-JUL-2000; 2000US-0216446P.	
XX	(ZYMO) ZYMOGENETICS INC.	
XX	Gao Z;	
XX	WPI; 2002-179701/23.	
XX	New murine cytokine receptor, Zcytor14, and polynucleotides encoding the	
PT	receptor, useful for treating inflammation, specifically rheumatoid	
PT	arthritis, and as educational tools or in research.	
XX	Disclosure; Page 98-99; 99pp; English.	
XX	The invention relates to murine cytokine receptor, Zcytor14. The Zcytor14	
CC	polypeptide is useful for identifying or isolating Zcytor14 ligands, in	
CC	preparing antibodies, in identifying proteins or peptide cleavage sites,	
CC	in amino acid sequence analysis, and in monitoring biological activities	
CC	of both the native and tagged protein in vitro or in vivo. Polypeptides	
CC	having Zcytor14 activity can be used to treat inflammation, such as	
CC	rheumatoid arthritis. Zcytor14 polynucleotide may be used as educational	
CC	tool in genetics, molecular biology, protein chemistry and antibody	
CC	production analysis, in the preparation of expression constructs for	
CC	bacterial, viral or mammalian expression, in determining mRNA and DNA	
CC	localisation of Zcytor14 polynucleotide in tissues, for identifying	
CC	related polynucleotides and polypeptides by nucleic acid hybridisation,	
CC	in linkage-based testing for various diseases in murine models, and to	
CC	determine whether a subject's chromosomes contain a mutation in the	
CC	Zcytor14 gene. Zcytor14 oligonucleotide probes are useful for in vivo	
CC	diagnosis, and for detecting and localising Zcytor14 gene expression in	
CC	tissue samples. The present sequence is human cytokine receptor, Zcytor14	
CC	which can be used to generate humanised variant of murine Zcytor14	
CC	sequence	
XX		
SQ	Sequence 692 AA;	
	Query Match 65.38; Score 2352.5; DB 5; Length 692;	
	Best Local Similarity 67.48; Pred. No. 2e-216;	
	Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;	
Qy	1 MPVSWFLSLALGRNPVVSLESLRMSQDPTARCSGLSLCHLWDGVLCLPGLSQSPGPV 60	
Db	1 MPVPWFLLSLALGRSPVLSLESLRVGPDQATHCSPLGSLCLMSDILCLPGLDVPAPGPV 60	
Qy	61 LVFRLQTELVLRCQKTDCLALRVVVVHLAVHGHWAEPPE---ACKSDSEIQESNAS 116	
Db	61 LAPTHLQTELVLRCQKETDCDCLRLVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS 120	
Qy	117 LQAQVLSFQAYPTARCALLEVQPADLVQPGQSGVSAVDFCEASIGASVQIWSYTKPR 176	
Db	121 LQAQVLSFQAYPTARCALLEVQPADLVQPGQSGVSAVDFCEALGSEVRIMSYTQPR 180	
Qy	177 YQKEINLTQQLP-----DGNVLLTLDVSEQDFSLLYLRPVPDALKSLWYKNLT 227	
Db	181 YKEINHTQQLPALPWLNVSDGNVHLVNVSEQHFGLSLYNVQVQGPPEKPRWKNLT 240	
Qy	228 GPQNTLNHTDLVPLCLCIQVMSLEPDSERVEFCFFREDPGAHRNLWHLARLVLSPGVWQ 287	
Db	241 GPQIITLNHTDLVPLCLCIQVWPLEPDSVRVNICPFREDPRAHQNLWQAARLRLTLQSWL 300	

Qy	288	LDAPCCILPGKVTLCWQAPDQSPQPLVPPVPPQKNATVNEPQDFOLVAGHPNLCVQVSTWE	347
Db	301	LDAPCSLPAAALCWRAFGDPCQPLVPPLSWENVTVDKVLEPFLKKGHPNLCVQVNSSE	360
Qy	348	KVQLQACSWADSLGPFKDDMLLVEMTKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEEL	407
Db	361	KLQLQECLWADSLGFLKDDVLLLETRGPQDNRSLSALEPSGCTSLPSKASTRAARLGEYL	420
Qy	408	LQDFRSHQWQNLANDDNMGSWACPMDKYTHRWVVLVWLAACLLLAALFFPLLLKKDRRK	467
Db	421	LQDLQSGQCLQLW-DDDLGALWACPMDKYTHKRWALVWLAACLLPAAALSILLKKDHAK	479
Qy	468	AARGSRITALLHSADGAGYERLVGALASALSQMLPRVAVDLWSRRELSSAHGALAWFHQR	527
Db	480	AAARGRAALLYSADDSGPERLVGALASALCOLPLRVAVDLWSRRELSSAQGPVAFWFAQR	539
Qy	528	RRILQEGGVILLFSPAAVAQCOQWLQQTVEP---GPHDALAAWLSCVLPDFLQGRATG	584
Db	540	QRTLQEGGVVLLFSPGAVALCSEWLQDGVSGCAHGHDAFRASLSCVLPDFLQGRAPG	599
Qy	585	RYVGWVFDGLLHPDSVPSRPAFLSLPTQLPAFLDALQGGCSTSAGRPADRVERTQA	644
Db	600	SYVGACFDRLLHPDAVPALEFRVFTPLPSQLPDFLQALQOPRAPRSGRLQERAEQVSR	659
Qy	645	LRGALDSC--TSSSEAPG 660	
Db	660	LQPALDSYFHPGCTPAPG 677	

RESULT 11	
ABW01911	
ID	ABW01911 standard; protein; 692 AA.
XX	AC ABW01911;
XX	12-FEB-2004 (first entry)
DE	Human cytokine receptor Zcytor14.
KW	Cytokine receptor; Zcytor14; cardiomyopathy; xeroderma pigmentosum;
KW	Marfan-like connective tissue disorder; diabetes mellitus;
KW	Fanconi anaemia; renal cell carcinoma; Marfan syndrome;
KW	Von Hippel-Lindau syndrome; blepharophimosis; human.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
Peptide	1..20
Protein	/label= Signal_peptide
Domain	21..692
Domain	/label= Mature_Zcytor14
Domain	21..452
Domain	/label= Extracellular_domain
Domain	453..473
Domain	/label= Transmembrane_domain
Domain	474..677
Domain	/label= Intracellular_domain
US2003199041-A1.	
23-OCT-2003.	
10-JUN-2003; 2003US-00458647.	
07-JUL-1999; 99US-0142555P.	
30-JUN-2000; 2000US-00608918.	
(PRES/) PRESNELL S R.	
(BURK/) BURKHED S K.	
(POWN/) POWNER S L.	
Presnell SR, Burkhead SK, Pownder SL;	

XX	WPI; 2003-852791/79.
DR	N-PSDB; AAD47894.
XX	New zcytor14 polypeptides, useful for treating xeroderma pigmentosum,
PT	Morfan-like connective tissue disorder, cardiomyopathy, diabetes
PT	mellitus, Fanconi anemia, renal cell carcinoma and Morfan syndrome.
XX	Claim 1; SEQ ID NO 2; Opp: English.
XX	The invention relates to human cytokine receptor Zcytor14 polypeptide and
CC	polynucleotide. The Zcytor14 polypeptide, polynucleotide and antibody are
CC	useful for treating xeroderma pigmentosum, Marfan-like connective tissue
CC	disorder, cardiomyopathy, diabetes mellitus, Fanconi anaemia, renal cell
CC	carcinoma, Morfan syndrome, Von Hippel-Lindau syndrome, or
CC	blepharophimosis. The present sequence is human cytokine receptor
CC	Zcytor14
XX	Sequence 692 AA;
OS	Query Match 65.3%; Score 2352.5; DB 7; Length 692;
XX	Best Local Similarity 67.4%; Pred. No. 2e-216;
XX	Matches 457; Conservative
QY	1 MPVNFLLSLALGRNPFVWSLERLMEPDPTARCSLGISCHLWDGDLCLPGLSQAPGPV 60
Db	1 MPVPWFLLSLALGRSPVLSLRVLPQDATHCPGLSCRLWDSLDLCLPGDIVPAGPV 60
QY	61 LVPTRLOTELVRCPKTDCAIRVVVHLAVHGHWAEP-----AGKSDSELQSRNAS 116
Db	61 LAPTHLOTELVRCKETDCDLRVAHVLAHVGHWEPEDEKEFGGAADSGVEEPRNAS 120
QY	117 LOAQVVLGFQAYPTARCALLEVQPADLVQPGQSVGSADVDFCEASIGAEVQIWSYTKPR 176
Db	121 LOAQVVLGFQAYPTARCALLEVQPADLVQPGQSVGSADVDFCEASIGAEVQIWSYTKPR 180
QY	177 YOKELNLTOQLP-----DGDNVLTLLDVSEQDFSLLYRPVDPDALSKLWTKILT 227
Db	181 YEKELNLTOQLPALPWLNVNSADGNVHLVNVSEHQHGLSLYNVNQVGPKPRWHKNUT 240
QY	228 GPONITLNTDVLPCICIQVNSLEPDSRVFECPPREDPGAHRLMHIARLRLVLSPGVMQ 287
Db	241 GPQITLNTDVLPCICIQVNPEDPSRVFNICFPREDPRAHQLMQAARLLTLTQSWL 300
QY	288 LDAPCCLPGKVTLQWAPDQSPQCPLVPPVFKQATNEPODQOLVAGHPNLCVOYSTWE 347
Db	301 LDAPCCLPAEMALCWAPCGDPCQLVPPFLSMENVTVDKLFEPFLKGHPNLCVQNSSE 360
QY	348 KVQLQACWADSILGPKDMILVEMKTGINNTVSICALPSPGCTPLPMSASTRAARLGEEL 407
Db	361 KLQLQECWADSILGPKDKDDVLLLETGTQPNRSICALPSPGCTSLPSKASTRAARLGEYL 420
QY	408 LQDFRSHOCMLNDNDNMGSLMACPMKYIHRRWLVLMACLLLAALFFFLILLKKDRRK 467
Db	421 LQDLQSQCQLQW-DDDLGLAWACPMKYIKRWLVLMACLLFAAALLSLILLKKDHAK 479
QY	468 AARGSTRALLHGADGAGYERIVGALASALCOMPLERVAVDLWSRELSAHGALAFFFHOR 527
Db	480 AARGGRAALLYSADDGGFERLVGALASALCOLPLERVAVDLWSRELSAQGVAFWFAQR 539
QY	528 RRILQEGGVVLLFPSAAVACQQWQLQQTVEP---GPHDAALWLSVLPDFFLOGRATG 584
Db	540 RQTLQEGGVVLLFPSGVALCVSEWLQDGVSGFGAHPHDPAFRALSCLVLPDFFLOGRAPG 599
QY	595 RYGVYFDGLLHDPDSVSPFRVAPLSLTPQLPAFTDALQGCGSTSAGRPADRVERVTAQA 644
Db	600 SYVGACFDRLLHDPDAVFALFRTVPFTLPSQLPDLFCALQQPAPRPSGRLQERARQVSR 659
QY	645 LRSLDSC--TSSEAPG 660
Db	660 LQPALDSYFHPPGTPAPG 677

Best Local Similarity 67.4%; Pred. No. 2e-216;
Matches 457; Conservative 66; Mismatches 136; Indels 19; Gaps 5;

QY 1 MPVSWFLSLALGRNPVVSLEPMDTARCSLSGLWGDVLCPLGSLQSPGPV 60
DB 1 MPVSWFLSLALGRNPVVSLEPMDTARCSLSGLWGDVLCPLGSLQSPGPV 60

QY 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEE-AGKSDSELOESRNAS 116
DB 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEE-AGKSDSELOESRNAS 120

QY 117 LQAOVLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPR 176
DB 121 LQAOVLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPR 180

QY 177 YOKELNLTQQLP-----DGNVLLTLDVSEEDPFLYLRLRPVDPALKSLWYKNLT 227
DB 181 YOKELNLTQQLP-----DGNVLLTLDVSEEDPFLYLRLRPVDPALKSLWYKNLT 240

QY 228 GPQNTLHTDLVPLCLCIQVMSLEPDSERVFPCFPREDPGAHRLMHIARLVLSPGVWQ 287
DB 241 GPQNTLHTDLVPLCLCIQVMSLEPDSERVFPCFPREDPGAHRLMHIARLVLSPGVWQ 300

QY 288 LDAPCCLPGKVTLCQAPDQSPCQPLVPPVPPQKNATVNEPQDFOLVAGHNPCLVQVSTWE 347
DB 301 LDAPCCLPGKVTLCQAPDQSPCQPLVPPVPPQKNATVNEPQDFOLVAGHNPCLVQVSTWE 360

QY 348 KYOLOACSWADSLGPPKDDMLVEMKTGLNNTSVCALEPSCCTPLPSMASTRARLGEEL 407
DB 361 KYOLOACSWADSLGPPKDDMLVEMKTGLNNTSVCALEPSCCTPLPSMASTRARLGEEL 420

QY 408 LQPRSHQCMLQNDNMGSLWACPMCKYTHRRVVLVWLACLLIAAALFFFLLLKKDRK 467
DB 421 LQPRSHQCMLQNDNMGSLWACPMCKYTHRRVVLVWLACLLIAAALFFFLLLKKDRK 479

QY 468 AARGSPALLHLSADGAGYERLVGALASLQMPPLRVAVDLWSRRRLSAHGALEWPHQR 527
DB 480 AARGSPALLHLSADGAGYERLVGALASLQMPPLRVAVDLWSRRRLSAHGALEWPHQR 539

QY 528 RRLQEGGVLLPESPAVACQWLOLQVTEP---GPHALAAWLSVLPDFLQBRATG 584
DB 540 RRLQEGGVLLPESPAVACQWLOLQVTEP---GPHALAAWLSVLPDFLQBRATG 599

QY 585 RYVGVVFDGLHPDSVPSRPAFLPSLTQPLAFDALQCGGSTAGRADRVRTVOA 644
DB 600 RYVGVVFDGLHPDSVPSRPAFLPSLTQPLAFDALQCGGSTAGRADRVRTVOA 659

QY 645 LRSALDSC--TSSSEAPG 660
DB 660 LRSALDSC--TSSSEAPG 677

RESULT 13
AEF05374
ID AEF05374 standard; protein; 449 AA.

XX AC AEF05374;
XX AC AEF05374;
XX DT 23-FEB-2006 (first entry)
XX DE Mouse zcytor14 extracellular ligand-binding domain.

XX antiinflammatory; antiasthmatic; gastrointestinal-gen.; antiulcer;
XX antiarthritic; dermatological; antipsoriatic; antibacterial;
XX immunosuppressive; antimicrobial; substrate inhibition; therapeutic;
XX inflammatory bowel disease; asthma; respiratory disease;
XX ulcerative colitis; antiulcer; Crohn's disease; gastrointestinal-gen.;
XX gastrointestinal disease; arthritis; antiarthritic;
XX musculoskeletal disease; psoriasis; antipsoriatic;
XX dermatological disease; immune disorder; atopic dermatitis;
XX dermatological; endotoxemia; inflammation; endotoxic shock; sepsis;
XX antibacterial; immunosuppressive; infection; zcytor14; receptor;
XX ligand binding domain.

XX OS Mus musculus.
XX PN W02005123778-A2.
XX PD 29-DEC-2005.
XX PF 10-JUN-2005; 2005WO-US020521.
XX PG 10-JUN-2004; 2004US-0578805P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Presnell SR, Burkhead SK, Levin SD, Kuestner RE, Gao Z;
PI Jaspers SR, Billeborough J;
XX PF1; 2006-067457/07.
XX New isolated soluble receptor comprises at least one Zcytor14 subunit,
XX useful for treating an inflammatory disease, e.g. asthma, inflammatory,
XX bowel disease, ulcerative colitis, arthritis, atopic dermatitis, or
XX psoriasis.
XX Disclosure; SEQ ID NO 27; 205pp; English.
XX The invention describes an isolated soluble receptor comprises at least
XX one Zcytor14 subunit, where the Zcytor14 subunit comprises a polypeptide
XX comprising fully defined 432 amino acids (SEQ ID NO. 3) or comprises
XX amino acid residues 1-427 of a fully defined 667 amino acid sequence (SEQ
XX ID NO. 24) given in the specification. Also described are: an isolated
XX soluble receptor comprising Zcytor14, where Zcytor14 comprises a
XX polypeptide having SEQ ID NO. 3; and where the soluble receptor reduces
XX the pro-inflammatory activity of either IL-17A comprising fully defined 153
XX amino acids (SEQ ID NO. 14) or IL-17F comprising fully defined 153
XX amino acids (SEQ ID NO. 16); an antibody or antibody fragment that binds
XX to a polypeptide comprising fully defined 692 amino acids (SEQ ID NO. 2),
XX and where the antibody or antibody fragment reduces the pro-inflammatory
XX activity of either IL-17A (SEQ ID NO. 14) or IL-17F (SEQ ID NO. 16);
XX reducing IL-17A-induced or IL-17F-induced inflammation; treating a mammal
XX afflicted with an inflammatory disease in which IL-17A or IL-17F plays a
XX role; and treating a pathological condition in a subject associated with
XX Zcytor14 activity. The soluble receptor comprising at least one Zcytor14
XX subunit is useful for treating an inflammatory disease, e.g. asthma;
XX chronic inflammatory disease selected from inflammatory bowel disease,
XX ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis, or
XX psoriasis; or acute inflammatory disease selected from endotoxemia,
XX septicemia, toxic shock syndrome, or infectious disease. This is the
XX amino acid sequence of mouse IL-17A and IL-17F receptor zcytor14
XX extracellular ligand-binding domain.
XX Sequence 449 AA;

Query Match 65.1%; Score 2348.5; DB 10; Length 449;
Best Local Similarity 97.6%; Pred. No. 2.4e-216;
Matches 438; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

QY 1 MPVSWFLSLALGRNPVVSLEPMDTARCSLSGLWGDVLCPLGSLQSPGPV 60
DB 1 MPVSWFLSLALGRNPVVSLEPMDTARCSLSGLWGDVLCPLGSLQSPGPV 60

QY 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEEAGKSDSELOESRNASLQAO 120
DB 61 LVPTRQLTELVLRCPOKTDICALRVVVVHLAVHGHWAEPPEEAGKSDSELOESRNASLQAO 120

QY 121 VLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180
DB 121 VLSFOAYPTARCALLLEVQVPADLVQPGQSVGSAVDFCFEASLGAEVQIWSYTKPRYQKE 180

QY 181 LNTLQQLP-----DGNVLLTLDVSEEDPFLYLRLRPVDPALKSLWYKNLTGPQN 231
DB 181 LNTLQQLP-----DGNVLLTLDVSEEDPFLYLRLRPVDPALKSLWYKNLTGPQN 240

QY 232 ITLNHTDLVPLCLCIQVMSLEPDSERVFPCFPREDPGAHRLMHIARLVLSPGVWQLDAP 291

Db 241 ITLHNTDLVPCLCIQWSLEPDSERFPCPREDPGARNLWHLARLVLSPGVQLDAP 300
Qy 292 CCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHNLGVQVSTWVKQL 351
Db 301 CCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHNLGVQVSTWVKQL 360
Qy 352 QACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRAGRELLQDF 411
Db 361 QACLWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRAGRELLQDF 420
Qy 412 RSHOCMLWNNDDNMGSLWACPMCKYIHR 440
Db 421 RSHOCMLWNNDDNMGSLWACPMCKYIHR 449
RESULT 14
ID AAB61884
XX AAB61884 standard; protein; 705 AA.
AC AAB61884;
DT 08-MAY-2001 (first entry)
XX Chimeric Zcytor14 protein #2.
DE Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antinflammatory; gene therapy; vaccine.
XX Homo sapiens.
OS WO200104304-A1.
PN 18-JAN-2001.
PD 30-JUN-2000; 2000WO-US018383.
PF 07-JUL-1999; 99US-00348854.
PR (ZYMO) ZYMOGENETICS INC.
PA Presnell SR, Burkhead SK, Powder SL,
PI WPI; 2001-112618/12.
DR New polypeptide encoding a human cytokine receptor Zcytor14, for treating
PT inflammation e.g. rheumatoid arthritis.
XX Claim 2; Page 105-107; 112pp; English.
XX The invention provides a new human cytokine receptor designated Zcytor14.
CC Zcytor14 can be expressed by standard recombinant methodology. The
CC encoding nucleic acid is useful for detecting the expression of a
CC Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC used to screen biological samples in vitro for the presence of Zcytor14.
CC Proteins, polypeptides and peptides having Zcytor14 activity can be
CC administered to a subject who lacks an adequate amount of this
CC polypeptide, for treating inflammation and conditions such as rheumatoid
CC arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC antibodies) can be used to treat a subject who produces an excess of
CC Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC Zcytor14 to a subject.
CC Zcytor14 protein
XX Sequence 705 AA;
SQ Query Match 64.9%; Score 2339; DB 4; Length 705;
Best Local Similarity 66.3%; Pred. No. 4e-215;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;
Qy 1 MPVSWFLSLALGRNPVVVSLERLWEPQDTARCSGLSLCHLWDGVLCLPGSLQSPGV 60
Db 1 MPVSWFLSLALGRNPVVVSLERLWEPQDTARCSGLSLCHLWDGVLCLPGDIVPAGPV 60

Qy 61 LVETRLQTELVLRCPOKTCALRRVVRVHLAVHGHABPEE-----ACKSDSELOESRNAS 116
Db 61 LAPTHLQTELVLRCQKEDCDLCLRVAVHLAVHGHABPEEEDKEKFGGAADSGVEPRNAS 120
Qy 117 LQAVVLSFOAYIARCALELVOPADLVOPGOSVGSVAVDFCFEASLGAEVQWISYTKPR 176
Db 121 LQAVVLSFOAYIARCALELVOPADLVOPGOSVGSVAVDFCFEASLGAEVQWISYTKPR 180
Qy 177 YQELNLTQLP-----DGDNVLTLTLDVSEEQDFSLLYLRPVDPDALKSLWYNLT 227
Db 181 YQELNLTQLPALPWLNVSDGDNVHLVLNVEEQHFGLSLYWNVQGGPKRWKHNLT 240
Qy 228 GPQNTLNHTDLVPCLCIQWSLEPDSERFPCPREDPGARNLWHLARLVLSPGVQ 287
Db 241 GPQNTLNHTDLVPCLCIQWSLEPDSERFPCPREDPGARNLWHLARLVLSPGVQ 300
Qy 288 LDAPCCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHNLGVQVSTW 347
Db 301 LDAPCCLPGKVTLCWQADQSPQCLVPPVPOKNAVNEPQDFQVAGHNLGVQVSTW 360
Qy 348 KVLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRAGRELL 407
Db 361 KVLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRAGRELL 420
Qy 408 LQDFRSHOCMLWNNDDNMGSLWACPMCKYIHRVWLVWLACLLLAALFFFLLLKDKRRK 467
Db 421 LQDFRSHOCMLWNNDDNMGSLWACPMCKYIHRVWLVWLACLLLAALFFFLLLKDKRRK 479
Qy 468 -----AARGSTRALLHSDAGYERLVGALASALQSMPLRVAVDLWSRRE 513
Db 480 GWRLRLKQDVESGAAARG-RAALLLYSADDSGFERLVGALASALQSMPLRVAVDLWSRRE 538
Qy 514 LSAHGALEWTFHQRRLILOEGVVLLESPAAVACQOVLQVPEP---GPHDALAAWL 570
Db 539 LSAQGFVAFWFAQRRTLOEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASL 598
Qy 571 SCVLPDFLQGRATGRYGVYFDGLIHPDSVSPFRVAPLFLSLPTQLPAFLDALQGCSTS 630
Db 599 SCVLPDFLQGRATGRYGVYFDGLIHPDSVSPFRVAPLFLSLPTQLPAFLDALQGCSTS 658
Qy 631 AGRPADRVERTQALRSALDSC--TSSEAPG 660
Db 659 SGRLQERAEQVSRALQPALDSYFHPGTPAG 690
RESULT 15
ID AAU29322 standard; protein; 705 AA.
XX AAU29322;
AC AAU29322;
DT 18-DEC-2001 (first entry)
XX Human PRO polypeptide sequence #299.
DE PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX Homo sapiens.
OS WO200168848-A2.
PN 20-SEP-2001.
PD 28-FEB-2001; 2001WO-US006520.
PF 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.

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OM protein - protein search, using sw model

Run on: August 16, 2006, 11:41:17 ; Search time 44 Seconds
(without alignments)
1473.866 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MPVSWFLSLALGRNPVVS.....SSEAPGCCSEWDLPCTTLE 674
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	3.2	267	2 A38442	probable tumor sup
2	114.5	3.2	1013	2 B70841	probable helz prot
3	110	3.1	2910	2 T42214	ocogelin - mouse
4	108.5	3.0	361	2 T39784	hypothetical prote
5	106.5	3.0	478	2 D75564	hypothetical prote
6	105.5	2.9	698	2 A82593	hypothetical prote
7	105.5	2.9	1451	2 B41185	alpha-2 macroglobu
8	105	2.9	1615	2 B49502	protein-tyrosine-p
9	105	2.9	1767	2 A49502	protein-tyrosine-p
10	103.5	2.9	3707	2 S18252	heparan sulfate pr
11	103	2.9	851	2 T31520	hypothetical prote
12	103	2.9	906	2 G83156	probable transcrip
13	102.5	2.8	1711	1 A55148	protein-tyrosine-p
14	101.5	2.8	1476	2 A41185	alpha-2 macroglobu
15	100	2.8	1447	2 A54100	tumor suppressor p
16	99.5	2.8	2647	2 T37098	gelation factor AB
17	99	2.7	1617	2 T28153	complement C4 - ch
18	99	2.7	2437	2 S42612	transmembrane prot
19	99	2.7	3014	1 JC5620	genome polyprotein
20	98.5	2.7	665	2 S69222	probable transcrip
21	98	2.7	824	2 H85498	helicase, ATP-depe
22	98	2.7	824	2 H90647	ATP-dependent heli
23	97.5	2.7	1618	2 S21424	nestin - human
24	97.5	2.7	1763	2 T17465	rifamycin polyketi
25	97.5	2.7	1894	2 C54689	protein-tyrosine-p
26	97.5	2.7	2629	2 T30987	telomerase-associat
27	97	2.7	604	2 G83091	conserved hypothet
28	97	2.7	963	2 T09478	ubiquitin thiolest
29	96.5	2.7	813	2 AF0526	ATP-dependent heli

30 96.5 2.7 1187 2 JE0347 hypothetical prote
31 96.5 2.7 1691 1 D54689 protein-tyrosine-p
32 96.5 2.7 2535 2 T04824 hypothetical prote
33 96 2.7 564 2 D96017 probable peptidase
34 95 2.6 1573 2 S01845 DNA (cytosine-5)-
35 95 2.6 10223 2 T30225 polyketide synthas
36 94.5 2.6 445 2 E70854 probable membrane
37 94.5 2.6 837 2 A34898 granulocyte colony
38 94.5 2.6 6260 2 T30228 polyketide synthas
39 94 2.6 509 2 JC5288 SHP substrate-1 pr
40 94 2.6 513 2 JC5289 SHP substrate-1 pr
41 93.5 2.6 527 2 A48085 transcription fact
42 93.5 2.6 1513 2 T23681 hypothetical prote
43 93.5 2.6 6831 2 A88852 protein unc-22 [im
44 93.5 2.6 6839 2 S57242 twichin [swilari
45 93.5 2.6 7160 2 T27935 hypothetical prote

ALIGNMENTS

RESULT 1
A38442
probable tumor suppressor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Feb-1997
C:Accession: A38442
R:Nigro, J.M.; Cho, K.R.; Fearon, E.R.; Kern, S.E.; Ruppert, J.M.; Oliner, J.D.; Kinzler
Cell 64, 607-613, 1991
A:Title: Scrambled exons.
A:Reference number: A38442; MUID:91121517; PMID:1991322
A:Accession: A38442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 >NIG>
A:Cross-references: UNIPARC:UPI000017C31D; GB:M63696; GB:M63700; GB:M63702; GB:M63718; GI
C:Keywords: transmembrane protein

Query Match 3.2%; Score 116; DB 2; Length 267;
Best Local Similarity 25.6%; Pred. No. 0.14;
Matches 72; Conservative 31; Mismatches 100; Indels 78; Gaps 16;

QY 155 VDFCFEASIGAEVQISYTKPRYQKELNLTQQLPD-----GDNVLTLDVSEQDFSL 209
DB 8 LVQC-EASLGDGSGSIISRTAKVAVAPLRPLSQTESVAFMGDTVLKCEVGE----- 59
QY 210 YLRVPDALKSLWYNLTGPQNTLNHTD-----LVPCLCIQWLSLEPDSERVEFCPPRED 265
DB 60 ---PMFTI---HWQKN---QQDLTPIGDSRVVVLPSGALQISRLQPGDIGYRCSAR-N 109
QY 266 PGAHENLWHIARLRLVLSPCVMOLDAPCCLPKVTLCWQAPD-OSPCQPLVPPVP-----OK 320
DB 110 PASSRT-GNEAEVRILSP-PWELNHPNL-----YAYESMDIEFFECTVSGKVPVTNNWMK 162
QY 321 NATVNEPQDFQLVAGHPNLGVQVSTWEKVLQACSWADSLGPPFKDD-----MLIVENKTGL 376
DB 163 NGDVVIPSDFQIVGSGNLRI-----LGVKSDGEGFYQCVAENAGN 204
QY 377 NNTSVCALEPSGCTPLPS-----MASTRAARL 403
DB 205 AQTSAQLIVPK---DIPSSSVLPSPAPRDVVPVLVSSRFVRL 242

RESULT 2
B70841
probable helz protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: B70841
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70841

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-1013 <COL>
A;Cross-references: UNIPROT:O53499; UNIPARC:UPI00000D7368; GB:AL021924; GB:AL123456; NID
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: hcz

Query Match 3.2%; Score 114.5; DB 2; Length 1013;
Best Local Similarity 20.4%; Pred. No. 0.97;
Matches 143; Conservative 75; Mismatches 232; Indels 251; Gaps 33;

QY 90 LAVHCHWAEP--EEAGKSGELOSERNASLQAQVLSFQAVPIARCALLEVQVADL--- 144

DB 2 LVLFHGFNSGGMRLWADSLL---VKSPQALRSARPHFA-----APADLLAG 49

QY 145 VQPGSGVSAVFDCFEASIGAEVQIWSYTKPRYQKELNLTOQLPDGDNVLLTLDVSEBQD 204

DB 50 IHPGK-----PATAVLLLPSSLSAPLD 71

QY 205 FSFLYLRLRPVDPALKSLMYKNLTGPQNTILNHTD-LVPCLCIQWLSLEPDSERVEFCFPR 263

DB 72 SPELTRLAPRAA-----RTDPMLLAWTPVVDLDPTAALAAFDQPA 113

QY 264 EDPGAHRLMHIARLRLVSPGWQLDAPCLPGKV-----TLGW---CAPDQS 308

DB 114 PDVRYGASVYLAEIAVARELVE-----RGRVLPQLRRDTHGAACWRPVLCGRDV 166

QY 309 PCQPLV---PPVPQKNATVNEPQDLVA-----GHPNLCVQ 342

DB 167 AWTSLVSAMPVPCRAEVGCHDPHELATSDAMDVAARAALSPMDLLPPRRGRSKHRA 226

QY 343 VSTW-----EKVQLOACS-----WAD-----SLGPFKDDMLLVEMKTLGNNTS 380

DB 227 VEAMLTALTCPDGRFDEPDLALAEALRPDDVIGTGVGPARTFRLSEVETENEET- 285

QY 381 VCALPSPGCTPLPMASTRAARLGBELLQDPRSHQW---OLWDDNMGSLWACPMCKY 436

DB 286 ---PAG-----SLWRL-RFLQSTQDPSLLVPAEQAWND--GSL----- 319

QY 437 IHRRWV---LVWLACLLAAALFFLLKKDORRKAAGSRFTALLHSGADGAGYERLVCA 492

DB 320 --RWLDRPQELLTELGRASRIFFELV-----PALRTACPSGLELDADGA--YRFLSG 369

QY 493 LASALSQMLPLRVAVDLWSRELSAHGALAWFHQRRTILOEGGVILLFSP--AAVAQCQ 550

DB 370 TAAVLDEAGFGVLLPSW-----W-----DRRRKL---GLVLSATVPDGVGVGKAS 411

QY 551 OWLQLOTVE-----PGPHDALAAWLSCVLP-----DFLQ 580

DB 412 KGRQLVEFRWELAVGDDPLSEEEIALTETKSPILRLRGQVVALDTEQMERGLEFLER 471

QY 581 RATGRVGVYFQGLL---HPDSVPSPRVPAPLSLPTQLPAFLDALOGGCGSTAGRAPDRV 638

DB 472 KPTGRKTTAEILALAAASHPDDVDTPLEVTAV-----RADGWLGDLLAGAAAALQFLDPP 526

QY 639 ERVTOALRSALDSCTS-----SSEAPGCCCEWDLGPCITLLE 674

DB 527 DGFTATLRPYQORGLAWLAFSLSGSLGSLADDMGLGKTVQ 567

RESULT 3

T42214

Ocogelin - mouse

N;Alternate names: mucin-like extracellular matrix protein

C;Species: Mus musculus (house mouse)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004

C;Accession: T42214

R;Cohen-Salmon, M.; El-Amraoui, A.; Leibovici, M.; Petit, C.

Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997

A;Title: Ocogelin: A glycoprotein specific to the acellular membranes of the inner ear.

A;Reference number: Z22079; MUID:98070772; PMID:9405633

A;Accession: T42214

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-2910 <CH>

A;Cross-references: UNIPROT:O52225; UNIPARC:UPI0000027C49; EMBL:U96411; NID:G2760883; PII

A;Experimental source: strain BALB/c

A;Note: Component of all the acellular membranes of the inner ear

C;Superfamily: von Willebrand factor

Query Match 3.1%; Score 110; DB 2; Length 2910;

Best Local Similarity 20.8%; Pred. No. 8.4;

Matches 54; Conservative 31; Mismatches 82; Indels 92; Gaps 13;

QY 214 VPDALKSLWYNKLAGPQNTILNHTDLVPCLCIQWLSLEPDS-----ERVEFCFPR 263

DB 2427 VPRALGETWNSLSG-----CCQCCQAPDTIIPVDLDCPGPRPESCP-- 2469

QY 264 EDPGAHRLMHIARLRLVSPGWQLDAPCLPGKVTLCQWADPQSPCPLVPPVQKNAT 323

DB 2470 -----RFGEVILLQP-----TEDPCCL-GSVCVC---NQFLCEGLAPTCRPGHSL 2510

QY 324 VNEPQDFOLVAGH-----PNLCVQVSTWEKVQLOACSADSLGPPKDDMLLVEMKTLGN 378

DB 2511 ITHQEDSCCPYSCECDPGLC-----EASQVPTC-----REQILLIEGRLG--- 2552

QY 379 TSVCALEPSGC---TPLPSMASTRA-----ARLGEELQDFRSHQ----- 415

DB 2553 DSCCTSYFCGCEGSDPMECEQEGEALTVHRNTTLCCLPQVCENFCRCPQVQCGMETS 2612

QY 416 CMQLWDDNMGSLWACPM 434

DB 2613 LVEVMSPRCCPYKSCCED 2631

RESULT 4

T39784

Hypothetical protein SPBC18H10.20c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T39784

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.

submitted to the EMBL Data Library, March 1998

A;Reference number: Z21879

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-361 <LYN>

A;Cross-references: UNIPROT:O60150; UNIPARC:UPI000006A75B; EMBL:AL022304; PIDN:CAA18417.1

A;Experimental source: strain 972h; cosmid c18H10

C;Genetics:

A;Gene: SPDB:SPBC18H10.20c

A;Map position: 2

Query Match 3.0%; Score 108.5; DB 2; Length 361;

Best Local Similarity 20.3%; Pred. No. 0.79;

Matches 84; Conservative 53; Mismatches 133; Indels 143; Gaps 21;

QY 16 PVVWSLERLMEPQDTCARCSLGLSCHLWDGDLVCLPGSLQSAFG-----PVL 61

DB 2 FLKALPRSTTPKDPARTLDIR--MESPPVLVFLGSPETSSGALASGILKLTILHQPFI 58

QY 62 VPTRLQTELVLRCPQKTDICALRVVVHLAVGHWAEPPEAGKSDSELSERNASLQAOV 121

DB 59 KVHTLKLQLIKRI-----TVLHPAI-SHCS-----ACAGSKEVLTQWDLAANTTY 102

QY 122 VLSFOAYPIARCALLEVQVADLVQPGQSGVSAVFDCFEASIGAEVQIWSYTKPRYQKEL 181

DB 103 RPTQHQWPPSW-----LFFGSLPASVSN-RYIKLEYLLEA 136

QY 182 NLTOQLPDGDNVLLTLDVSEBQDFSFLLYL-----VVPALKSLWYKNLTGPNITLNT 237


```
Db 137 TLCTGTPEGG-----ISPSKEVLEKFPQLKRAIAPSPDTI-----HKRIPTPTNLVANIT 187
Qy 238 DLVPCLCIQWISLEPDS---RVFPCFPREDPGAHRLNWHIARLVLSFGWQLDAPCCCL 294
Db 188 ---LFS-----TLPHGAALEVMVTGTFQAQDNG---NDWKINRV-----TWRLSEHM-- 228
Qy 295 PGKVTLCWQAPDQSPQCP-----LVPPVPQKNATVNEPQDFQVLVAGHPNLCVQVSTWEK 348
Db 229 -----QFSCQPCERHRLDVKPRPIEKRIILSTQDLQ-----SGWK- 263
Qy 349 VOLQACSWADSLGPFKDDMLVEMKTLGNNTSVCALESPSGCTPLPSPMASTRAA 401
Db 264 -----FIDNQMF--LSTQINTSSL--REPSCDVEIPAPFSLKVS 298

RESULT 5
D75564
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: D75564
R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75564
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-478 <WHI>
A:Cross-references: UNIPROT:Q9RY89; UNIPARC:UPI00000C16BA; GB:AE001869; GB:AE000513; NID
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0061
A:Map position: 1

Query Match 3.08; Score 106.5; DB 2; Length 478;
Best Local Similarity 23.28; Pred. No. 1.6; Mismatches 184; Indels 169; Gaps 23;
Matches 118; Conservative 38;

Qy 213 PVP---DALKSLMYKNLTGPNITLNHTDLVPCLCIQWISLEPDSERVEPCFPREDPGAH 269
Db 17 PVPAGDVLVSLGNSEVVRQLARTLGLDILLPGGAQVWQA---LDRVEDDFPPQPGDD 73
Qy 270 RNLWHIARLR-----VLSGV-----W----- 286
Db 74 ALFAQLAAIRQGGSPHERAQLBEVLRAGAGPQSALRADPRERPLLREAAQRIRRLARR 133
Qy 287 QLDAPCCCLGKVTLCWQAPDQSPQCPQPLVPVPQKNATVNEPQDFQVLVAGHPNLCVQVSTW 346
Db 134 LARAPQGLPTGTPAHSVLYAQEEASALSAPAGDGLTLH-----LGGPD---RLAHW 182
Qy 347 EKVOLOACSWADSLGPFKDDMLVEMKTLGNNTSVCALEPSGCTPLPSPMASTRAARLG 404
Db 183 QGLRL---SWR-SLGP--NQWLLVQDETSPVSGGQALLRPD---LP-ASER----- 225
Qy 405 EELLQDFRSHQCMQMLWDDNMGSLWACPMCKYIHRRWVLVWLACILLAAALFFPLLKCD 464
Db 226 -QLPLTVGGQQLVLPFGD-----YVLLRRR 250
Qy 465 -----RRKARGERTALLHSADGAGYERLVGALASALSQMPLRVAVDLWSRELS 515
Db 251 ADAAQTRHLARLAALGACALLLPABQHGRLRLARTLARLRGDP-----PRADDP 302
Qy 516 AHGALAWFH-----HQRRRLQGGVVILLFSPAAVAQCOQWLQLQTVBPGHDALAAW 569
Db 303 ASGVAVFAQTPAECIAARSLQRLBFLGFSFAQVA-----HEADVAQ 347
Qy 570 LSCVLPDFLOGRATGRVGVVFDGLLHPDSVPSPFRVA-----PLFSL---FTQLPA---FL 620
Db 348 ALLHLPP-----HYAAQVQQAEEAASAAEPLREAAATDPLVGREAGPPVLPATGHFI 399
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Qy 621 DALQGGCSTSGRPAADRVERVTQALRSAL 649
Db 400 VFPLGPPDPLEVRLPGDKLLTLRPDYRAEL 428

RESULT 6
A82593
hypothetical protein XP2169 (imported) - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82593
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen-
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: A82593
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <STM>
A:Cross-references: UNIPROT:Q9PBHS; UNIPARC:UPI00000C2968; GB:AE004030; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Pacinani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XP2169

Query Match 2.98; Score 105.5; DB 2; Length 698;
Best Local Similarity 20.48; Pred. No. 3.1;
Matches 142; Conservative 84; Mismatches 257; Indels 213; Gaps 34;

Qy 9 SLAAGNPVVVSLERLWE-----PDQTA-RCSGLSCHLWDGVDVLCPLGSLQSA--FGPV 60
Db 150 TIALRGQVDQATMLTSQAVELLPEEPVLFSLGFA-YLQKHIAFAERAPQVRIELNPH 208
Qy 61 LVPTRLQTELVLRCPQKTDCALRV-RVVVHL-----AVHGHWAEP-EAGKSDSEIQES 112
Db 209 VIPVRALIAQAQOGRGLDDALAILEALSIPSGDTPALHRLTGEFELLAGHPDRLATHL 268
Qy 113 RNASLAQAVVLSFOAVPIARCALLEVQVPADLVQPGSGVSAVDFCDCEASLGAEVQWSY 172
Db 269 R-----QVLATWPEDPRTLEALLTAWKQLDMDDDRITLDAALD----- 307
Qy 173 TKPRYQKELNLTQQLPDGDNVLTLDV-----SEEQDFSLLYLRPVPDALKSLMYKNLTG 228
Db 308 IKPR-----NHDLMTLARLAVAPVGSDEARIVIERVLSAMPEHLPAL--ETLMS 353
Qy 229 PONTILNHTDLPCLCIQVWSLEP-----DSERVEFCFPREDPGAHRLNWHIARLVLSPG 284
Db 354 LHDIQ-NPPEASTVARIQIVAIEPGLSGEQRIVEALLQDPPT----- 396
Qy 285 VWOLDAPCCCLPGKVTLCWQAPDQSPQCPPLVPVPQKNATVNEP-----QD-----FQLVAG 335
Db 397 ----AVACL-----QQLTESVEHERTILRPWLGLVQDRAGQFE---- 431
Qy 336 HPNLCVQVSTWEKVOIQACSWADSLGPFKDDMLVEMKTLGNNTSVCALESPSGCTPLPSPM 395
Db 432 ----AALATWLFQAEQAKYRLPLPP-----QTWNSKQ-----WPD 465
Qy 396 ASTRAARLGBELAQDFRSHQCMQMLWDDNMGSLWACPMCKYIHRRWVLVWLACILLAAAL 455
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Db 466 AAIAPAILARPELL-----INGPQSHVERVTMMWASSMLC----- 502
QY 456 FFFLLKKDKRKAARGSTALLHSADGAGYERLVGLASALSQMPLEAVDLWSRRELS 515
Db 503 -----ADRYSETP-----PADPLQRYETVSELTS--GTLTPQALIDAW-ROQLP 543
QY 516 AHGA-----LAWFHQ-----RRRILOEGGVILLSPRAVAQCQOQLQTVPEGPH 563
Db 544 ARGIEDGNVIDWLLWMDNSLLTALRPHLPEGRLLIIVLRDPRDM--LLDWIAYGSPILAL 601
QY 564 DAL---AAWLSVLPDFQGRATGRYGVYDGLLHPDSV-PSPRVA-----PLFSLPTQ 615
Db 602 DSLQQAANWLG-----DILNQIAALHELDLYPHLIRLDGIEDNPQALTTLEDIFGSPFP 657
QY 616 LPAFIDALQGGCSTAGRAPRVERVTOALRSALDS 651
Db 658 IPPSLEAPR-----LPAGRWRDYREVLSSAFDA 685
RESULT 7
B41185
alpha-2 macroglobulin homolog MUG2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text change 09-Jul-2004
C:Accession: B41185
R:Overbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
J. Biol. Chem. 266, 16903-16910, 1991
A:Title: Molecular characterization of the murinoglobulins.
A:Reference number: A41185; MUID:91358495; PMID:1840592
A:Accession: B41185
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1451 <OVS>
A:Cross-references: UNIPROT:P28666; UNIPARC:UPI0000028B3F; GB:M65238; NID:g199888; PIDN:
C:Superfamily: alpha-2-macroglobulin
Query Match 2.9%; Score 105.5; DB 2; Length 1451;
Best Local Similarity 20.4%; Pred. No. 7.9;
Matches 76; Conservative 48; Mismatches 159; Indels 89; Gaps 17;
QY 67 QTELVRCPQ-----KTPCALRVVVVHLAV-----HGHWAEPREA--- 102
Db 454 ETSSILPCNQIHTVQAHFTLKGLGVLKELVLYLWMAQSIITQGNHTHVEPGEAPVK 513
QY 103 GKSDSELOESRNASLQAVVLSFQAVPIARCALLEVQVPADLVQPGQSVGSVDFCFEAS 162
Db 514 GNFDLE-----IPVEFSMAPMAKMLIYITLPDGEVI--ADSVNFEIEKCLRNK 559
QY 163 LGAEVQIWSYTKRYQKELNLTQOLPDGDNVLTLDVSEEDFSFLLYLRPVPDALKSLW 222
Db 560 VDLSSFS--SQSLPASQTRLOQTAS--PQSLCGLRAVDQS-----VLLKXP-EDLSPSW 609
QY 223 YKMLTGPQNTLTHNTDLVP-----CLCIQVMSLEPDSERVFPCPPREDPGAHR-- 270
Db 610 IYNLPGMQ-----HNKFIPISSSI SEDREDICILVSSWAE---KHTDWVHGREDVYRYV 661
QY 271 ---NLWHIARLRLVSPGWQLDAPCCILP-GKVTLCWQAPDQSPQ-----PLVPPVPQK 320
Db 662 EDMDLKAFNTLKIPLKICFDSAPMSGPRGKFDLAFSEVSGTILQKGSKRPOPEEPRE 721
QY 321 NATVNEPQDFQLVAGHPNLCVQVSTWEKVQLQACSWA-----DSIGPFKDDMLLVEMK 373
Db 722 DPPPDKPLAETIRKYFFETWY----WDIVTVNSTGVAEVEMTVPTDITTEWKAGNGLCLNSD 777
QY 374 TGLNNTSVCALE 385
Db 778 TGLGLSSVVPFLQ 789
RESULT 8
B49502
protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type 4E, splice form B precursor - f

C:Species: Drosophila melanogaster
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: B49502
R:Oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A:Title: Alternative splicing in a novel tyrosine phosphatase gene (DPTP4E) of Drosophila
A:Reference number: A49502; MUID:94043220; PMID:8226938
A:Accession: B49502
A:Molecule type: mRNA
A:Residues: 1-1615 <OON>
A:Cross-references: UNIPROT:Q9W4F5; UNIPARC:UPI0000177053; GB:L20894
C:Genetics:
A:Gene: FlyBase:Pcp4E
A:Cross-references: FlyBase:FBgn0004368
A:Introns: 1605/3
C:Superfamily: protein-tyrosine-phosphatase, receptor type 4E, fibronectin type III repeat
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor
F:1254-1270/Domain: transmembrane #status predicted <TMN>
F:1271-1615/Domain: intracellular #status predicted <INT>
F:1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1531/Binding site: substrate phosphate (Arg) #status predicted
Query Match 2.9%; Score 105; DB 2; Length 1615;
Best Local Similarity 22.3%; Pred. No. 9.9;
Matches 98; Conservative 49; Mismatches 136; Indels 156; Gaps 26;
QY 60 VLVPTRLQTELVLRC-----PQKTDICALRVVVVHL-----AVGHWAEPREA 102
Db 403 ILEPGRTY-EVWVKTIADNVNVPASGEVTLRPRVPSLGGFLDDRSNALHLSW-EPAET 460
QY 103 GKSDS---ELOESRNAS-----LQAVVLSFQAVPI-----ARCALLEVQVPADLV 145
Db 461 GRQDSYRISYHEQTWASEVPAPVPAESQITNLTLYTLDLSLLAGRYLIAVQALS--- 517
QY 146 QPGQSVGSVDFCFEASLGAEVQIWSYTKRYQKELNLTQOLPDGDNVLT---TLDVSEE 202
Db 518 ---KGVASNASD-----ITRYTRP-----AAPLIQELRSIDQGLMLSWRSVDVNSR 559
QY 203 QP-----PSFLLYLRP-----VPDALKSLWYKNLTG-- 228
Db 560 ODREYVHYORNGTREERTWATNETSLTILHLPQSGYEVKVAISHGVSEPHSYFQAVF 619
QY 229 ---PQNTILN--HTDLVPCLCIQVMSLEPDS-----RVFPCFPREDPGAHRN--- 271
Db 620 PKPPQNLTLQTVHTNLV---VLHWQAPEGSDFSEYVWVRYRTDASFPQWRISGLHENEARI 675
QY 272 -----LWHIARLRLVSPGWQLDAPCCILPGKVTLCWQAPDQSPQPLVPPVPQKNATVN 325
Db 676 KDMHYGERYLQVNTVSGV---ESPFLPLELNVTM-----PPQ-PVSNVVPLVDSRNLITLE 727
QY 326 EPQDFQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPPFKDDMLLVEMK--TGLNNTSVCA 383
Db 728 WRP-----DGH-----VDFYTLKWPT-----DEEDRVEFKNVTQLEDLS--- 763
QY 384 LEPSGCTPLPMSASTRAAR 402
Db 764 -SPSVRIPIEDLSPGROYR 781
RESULT 9
A49502
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 4E, splice form A precursor -
C:Species: Drosophila melanogaster
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C:Accession: A49502
R:Oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A:Title: Alternative splicing in a novel tyrosine phosphatase gene (DPTP4E) of Drosophila
A:Reference number: A49502; MUID:94043220; PMID:8226938
A:Accession: A49502
A:Molecule type: mRNA
A:Residues: 1-1767 <OON>

A;Cross-references: UNIPROT:Q9W4F5; UNIPROT:Q24495; UNIPARC:UPI0000177052; GB:L20894
A;Note: authors translated the codon ATA for residue 1715 as Leu
C;Genetics:
A;Gene: ptp4E
A;Cross-references: FlyBase:FBgn0004368
C;Superfamily: fibronectin type III repeat homology; protein-tyrosine-phosphatase homol
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept
F;1254-1270/Domain: transmembrane #status predicted <TM>
F;1271-1767/Domain: intracellular #status predicted <INT>
F;1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1531/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.9%; Score 105; DB 2; Length 1767;
Best Local Similarity 22.3%; Pred. No. 11;
Matches 98; Conservative 49; Mismatches 136; Indels 156; Gaps 26;

QY 60 VLVPTRLQTELVLRC-----PKQDCLALRVVVHL-----AVGHWAPEEA 102
Db 403 ILPEGRKY-EVVVKTIADNVNSWPASGEVTLRPRVRSGLGGFLDRSNALHISW-EPAET 460

QY 103 GKSDS---ELQESRNAS-----LQAQVLSFQAYPI-----ARCALLEVQVPADLV 145
Db 461 GRQDSYRISYHEQTNASEVPAPFPAESQITNTLFTYLDLSLLAGRRYLIQVALS--- 517

QY 146 PQGQSVGSVDFCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDGDNVLL---TLDVSEE 202
Db 518 ---KGVASNASD---ITRYTRP---AAPLIQELRSIDQGLMWSRSDVNSR 559

QY 203 QD-----PFLLYLRP-----VPLAKSLWYKNTGT--- 228
Db 560 QDRYEHYQNRGTRERTWATNETSITIHLPGSGYEVKVAISHGVRSSEPHSYFQAVP 619

QY 229 ---PQNTILN---HTDLVPLCLIQWLSLEPDSE-----RVFCFPREDPGAHN--- 271
Db 620 PRPPQNLTLQTVTNLV-----VLHQAPEGSDSEVYVRYRTDASFWQISGLHNEARI 675

QY 272 -----LWHIARLRLVSPGWQDAPCCLPGLKVKTLQWAPDQSPCQPLVPPVPQKNATVN 325
Db 676 KDMHYGERYLQVNTVSFGV---ESPHLELVNTM---PPQ-PVSNVVLVDSRNLTLE 727

QY 326 BPQDFQVLVAGHPNLCVQVSTWEKVIQACSWADSLGFFKDDMLLVEMK---TGLNNTSVCA 383
Db 728 WPRP-----DGH-----VDFYTLKWWPT-----DEDRVFEKNVTQLEDLS--- 763

QY 384 LEPSCGCTPLPSMASTRAAR 402
Db 764 -SFSVRIPEDISPGQYR 781

RESULT 10
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 12-Jul-2004
R;Accession: S18252; A31917; B31917; S66460
J;Noonan, D.M.; Fullie, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogl
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NO>
A;Cross-references: UNIPROT:Q05793; UNIPARC:UPI00000278DD; EMBL:M77174; NID:g200295; PID
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hase
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>

A;Cross-references: UNIPARC:UPI000016CFA0; GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: UNIPARC:UPI000016CPA8; GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
A;Cross-references: UNIPARC:UPI000017C67C
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256, 1891, 2336, 2394, 2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.9%; Score 103.5; DB 2; Length 3707;
Best Local Similarity 20.5%; Pred. No. 37;
Matches 87; Conservative 44; Mismatches 167; Indels 127; Gaps 19;

QY 26 EPQDARCISLG-LSCHLW---DGDVLCPLGSLQS-----APGPVLVPTRLQTELVLRL--- 73
Db 326 ENEEPA-CENGHCALKWRCGDGDFCEDTDEANCSVKQGEVCGTFHFCVSTNRCIPA 384

QY 74 ---CPQKTCALRVVRVVHVLAVGHWAPEEAKSDSELSQESRNASLQAQVLSFQAYPI 130
Db 385 SFHCDEESDCPR-----SDFEGCMPQVVPVTPQSQIA----- 418

QY 131 ARCALLEVQVPADLVQPGQSVGSVDFCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDG 190
Db 419 -----SRGQTV---TFTCVATGVPTPIINRLNMGWHPAHPRVYTMTEGG 460

QY 191 DNVLLTLDVSEBQDFSFLL-----YLRPVPDALKSLWYKNTGTQPN---ITLNHTDLVP 241
Db 461 RGTLIIRDVKEADQAGYTCENNSRGWVFGIDGVLELVLPQRGPCPDGHFYLEDSASCLP 520

QY 242 CLCQVMSLEPDSEVFCFPREDPGAHNRLWHIARLRLVSPGWQDAPCCLPG-KVTL 300
Db 521 CFCFGVTVNCQSSLR-----PRD-----QIRL-----SFDQPNDFKGVNVTM 557

QY 301 CWQAPDQSPCQPLVPPVPQKNATVNEP-QDFQVLVAGHPNLCVQVSTWEKVIQACSWADS 359
Db 558 -----PSQGVVPLSSTQLQIDPALQEFQLVDLSRRFLVHDAPFWALPKQPLGNKVDS 609

QY 360 LGFFKDDMLLVEMKTLNNTSVCALEP-----SCTPL-PSMASTRAA 401
Db 610 YGFFLYRYKRYELARGM-----LEPVQKPDVILVAGYRLHSRGTHTHFGTLNQRV 662

QY 402 RLGESE 406
Db 663 QLSESE 667

RESULT 11
T31520
hypothetical protein Y116A8C.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
R;McMurray, A.
submitted to the EMBL Data Library, October 1999
A;Reference number: 221041

A;Accession: T31520		A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA		A;Residues: 1-851 <WIL>	
A;Cross-references: UNIPROT:Q9U2S3; UNIPARC:UPI000008020F; EMBL:AL117204; PIDN:CAB55154		A;Experimental source: clone Y116A8C	
C;Genetics:		A;Gene: CESP:Y116A8C.14	
A;Introns: 99/3; 124/2; 193/2; 225/3; 431/3; 660/2; 709/1; 795/3			
Query Match		2.9%; Score 103; DB 2; Length 851;	
Best Local Similarity		19.7%; Pred. No. 6.4; Indels 188; Gaps 34;	
Matches 114; Conservative 88; Mismatches 88			
QY	103	GKSDSELOESRNASLQAQVILSF-----QAYPIARCALLEVQVPAD	143
DB	41	GKQLFPFSAARHSIEAEFLSFNEEDAEKGTALPTWASIKRAGQPKTSVGNQILYD	100
QY	144	-LVQP-GQSVAGVDFCEASLGAEVQIWSYTKPRYQKELNLTQQLPDGDNVLLTLDYSE	201
DB	101	TLPOQRESIPSAIFNSFS-----NLKKGTPVSKRVNF-----	135
QY	202	EODFSFLVLRVPDALKSLWKNTGTQNTILNHTDLVPCLCIQWMSLEPDSERVEFCP	261
DB	136	QKSFPAKCKLRISWVA-----YAVN-----TIEHPDEA-----	176
QY	262	FREDPGAHNLWHIARLRLVLSFGVWQLDAPCCLPKGVTLCWQAPDQSPQCPVLPVPQKN	321
DB	177	ILENFENRRRIGVL--FSYLLP-VFNI-----LPSKTQ--QAPPTILINSIMPLTSKQK	225
QY	322	ATVNEPDQQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPKDKDMLLVEMKTLGNTNTSV	381
DB	226	PSLRSLSURL-----PDFSTEP-FPDFKHNCS-PDNVQPEE-----	262
QY	382	CALEPSCGCTPLFSMASTRARLGEELLQDF--RSHQCMQLMNDNMGSLWACPMKYI--	437
DB	263	--LAPSKITFPFKHICAR-----EELTRKFAKRVHDKIRVK--ANLWS-KTDQFLAM	310
QY	438	---HRRWLVWLA-----CLLIAAALFFLLLKDDRRKAAG-----SRTALLLHS	480
DB	311	GVDERPWFYTWISTVQTFVCIL--SLTFYGFAPFALEMEAREAGDVMDITLSSRVAYLSQ	368
QY	481	AD---GAGYERLV--GALASALSQMLRVAVDLWSRRELSAHCALAWFHRRRLIQEGG	535
DB	369	SNPWFPGHYADLIRLGAVSPC-----MRLELWKAIE-----EURLNKTG	412
QY	536	VVIL-----LFSPAQAQCCQWLQQLQTVFPG-----PHDAAALWLSCLVLPDFLQ	580
DB	413	CCITNDRSGCYQSSEISICPTWIRWIRWDKPLTAASKNFLTHTSKTIW-----TOP	464
QY	581	RATGRVGVYFDGLLHPDSVPSFVRVAPLPSLP--TQLP	617
DB	465	RKSGVCG-----QDPSCYRLFLSVAP-YENPDDSTQMP	497
RESULT 12			
G83156			
Probable transcription regulator PA3921 [imported] - Pseudomonas aeruginosa (strain PAO1)			
C;Species: Pseudomonas aeruginosa			
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004			
C;Accession: G83156			
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.			
Nature 406, 959-964, 2000			
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen			
A;Reference number: A82950; MUID:20437337; PMID:10984043			
A;Accession: G83156			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-906 <SRO>			
A;Cross-references: UNIPROT:Q9HX92; UNIPARC:UPI000000CSB79; GB:AE004091; NID			
A;Experimental source: strain PAO1			

C;Genetics:
A;Gene: PA3921
C;Superfamily: regulatory protein malt

Query Match 2.9%; Score 103; DB 2; Length 906;
Best Local Similarity 20.7%; Pred. No. 6.9; Indels 190; Gaps 23;
Matches 97; Conservative 45; Mismatches 136

QY 313 LVPVPQKNATVNEPDQQLVAGHPNLCVQVSTWEKVQLQACSWADSLGPKDKDMLLVEM 372

DB 348 LARLP-----DFGPSAG-----SLHRCAGWFSRHG-----LLDQ 378

QY 373 KTGLNNTSVCALEPSCGCTPLFSMASTRARLGEELLQDFRSHQCMQLMNDNMGSLWACP 432

DB 379 -----AVEQALRAGQPDVAASLVQNLSSEQLLAEQNIATLLRWKMDLPDLSLAST 428

QY 433 MDKYHRRWLVWLAALL-----LAAALFFFL-----LL-----KKD 464

DB 429 PRLLILYGALA-LACQLDAAABELAGQLARELPAPDESQAORDLLAQWQALSQVVIARGRD 487

QY 465 RRKAARSGRTALLHSADGAGVERLVGALASALSQMLRVAV---DLWSRRELSAHCAL- 520

DB 488 IDKAEAHCREAL-----QDLAG-ER-YGRLOCLSTLS-NLAVTRGDFWQARNYN-RDALE 539

QY 521 -----AWFHRRRLIQEGGV-----ILLF 541

DB 540 FAQRVGNPLFEALVHYDRARVLQARGEVARABEEVROGLERLQHLPAQRRYAVRGRLLLY 599

QY 542 SPAAVAQCCQWLQQLQTVFPGHDALAAMLS-----CVLPDFLQGRAT 583

DB 600 -----RGYLSLALQF---DEARKWIKOGIEETRCDVSLVIGYCVLAS-LEGR-L 646

QY 584 GRVGVY-----FDGLLHPDSVPSFVRVAPLPSLPQ----- 615

DB 647 GNVAAAFARLGDVERLMDANDIPPIYLYLAATILKELWLAQQLAGWQLQRLGGTYG 706

QY 616 -----LPAPLALQGCSTAGRPADRVERTVQALRSALDS 651

DB 707 GQATPPECSPLLPLHVELLQAGLERREGRPPEAAARLDRLARSTREN 754

RESULT 13

A55148

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat

N;Alternate names: OST-PTP; osteotesticular protein-tyrosine-phosphatase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A55148

R;Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.

J. Biol. Chem. 269, 30659-30667, 1994

A;Title: Identification of a hormonally regulated protein tyrosine phosphatase associated with the rat

A;Reference number: A55148; MUID:95074080; PMID:7527035

A;Accession: A55148

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1711 <MAU>

A;Cross-references: UNIPARC:UPI000004DC1D; GB:I36884

C;Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosin

C;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III repe

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prote

F;18/Domain: signal sequence #status predicted <SIG>

F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MAU>

F;1174-1398/Domain: protein-tyrosine-phosphatase homology <FPL>

F;1350/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.8%; Score 102.5; DB 1; Length 1711;
Best Local Similarity 20.6%; Pred. No. 17; Indels 267; Gaps 40;
Matches 149; Conservative 79; Mismatches 229

QY 43 DGDVLCPLGSLQSA-----PGVPLVPLRLQTEL-VLRCFPK-----TDC 80

DB 333 DGVVLKSGPMESTSLTGPEECNAVFPGP-LPPGHVTLQLKVLGAPYDAWVEGSTWLAES 391

Qy	81	ALRVRVVHLAVGHWAPEBZAKSDSELQSRNASLQAVVLSFQAVPIARCALLEVQV	140
Db	392	AALPREVEFGARL--WLDGLEASK--QPGRRALLYSD--DAPGSLGNISV	434
Qy	141	PADLVQ-----PQO-----SVGSAAVPCPEASLGAEVQIMSYTKPKRYKELNLTQQLPD	189
Db	435	PSGATHVIFCGLVPGAHYRVDIASGTDISGISG-----YTSFLPPQSLEV-----	481
Qy	190	GDNVLLTLDVSEBQDFSLLYLRPVDPDAL-----KSLWYKNLT-----GPQNITLHH	236
Db	482	-----ISRSPSDLTIAWGPAQGLEGVKVTWHQDGSQRSQCDGLVDLGPDTLSLT	532
Qy	237	TDLYP---CLCTQW---SLEPDSERVEFCP-----FREDPCAHRNLWH-----	274
Db	533	KSLVPGSSYTVSAWAGNAGTSDSQKIHSTRPAPTNLSLGFAGHQAALKASMYHPFGG	592
Qy	275	-----IARLRVL---SPGV-----W-QLDAPCCLPGKVTLCWOAPDQSPQPLV	314
Db	593	RDAPHRLRYLRPLTLESEKVLPREAQNFSNAQLTAGCFQVQLSTLWGSERS--	646
Qy	315	PPVPQKNATVNEPQDFQLVAGHPNLQCVSTWEKVQLQACSWADSLGFPFKDDMLLVMKT	374
Db	647	----SANATGWTP-----PSAPTL-VNVTSDAPTQLQV-SWAHPVG-----	681
Qy	375	GLNNTSVCALEPSGCTPLPSPNASTRARLGEHLLQDFRSHQCMQLWDDNMGSLWACPM	434
Db	682	GRSRYQVTLYOESTRTATSIINGP-----KEDGTSFLGLTFTGT	718
Qy	435	KYIHRRWVLVWLACLLAAA--LPPFLLKKDRRKAARSGRTALLLHLSADGAGYERLV-	490
Db	719	KY--KVEVISAQGLYTHAANVSATYPLIPNE-----LLVSMQAGSAVVNLAW	765
Qy	491	-----GALASALS-----QMPLRVADLWGSRRLSAHGALAFWHQRRRILQEGGV	536
Db	766	PSGPLGQACACHAQLSDAGHLSWEQPLKLGQBLFRLDLTPGHTISMSVRCRAGPLQASTH	825
Qy	537	VILLFSPAQAQCOOWLQOVTEGCP-HDAL-----AAMLS-----CVLPDFLQ	579
Db	826	LWL-----SVTEGPEVDVLCHEPTYALNWTMPAGDVVDVCLV-----	864
Qy	580	GRATGRVY---GVYF-----DGLLHPDSVP-SPPRVAPLFSLTLPOLPAFLDALOGCC	627
Db	865	--VVERLVPGGTHFVQVNTSGDALLPLNLMPTTSTYRLS--LTVLGNSRWSRAVSLVC	920
Qy	628	STSA	631
Db	921	STSA	924

RESULT 14

A41185
 alpha-2 macroglobulin MUG1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 12-Apr-1995
 C:Accession: A41185
 R:Overbergh, L.; Torrekens, S.; Van Leuven, F.; Van den Berghe, H.
 J. Biol. Chem. 266, 16903-16910, 1991
 A:Title: Molecular characterization of the murinoglobulins.
 A:Reference number: A41185; MUID:91358495; PMID:1840592
 A:Accession: A41185
 A:Status: preliminary
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1476 <OVE>
 A:Cross-references: UNIPARC:UPI0000176340; GB:M65736
 C:Superfamily: alpha-2-macroglobulin

	Query Match	2.8%	Score 101.5;	DB 2;	Length 1476;	
	Best Local Similarity	21.4%;	Pred. NO. 17;			
	Matches	72;	Conservative 44;	Mismatches 149;	Indels 71;	Gaps 16
Oy	86 VVHVLAV-----HGHWAEPEEA---GKSDSELOBSRNASLQAOVVLSFQAPYPIARCALLE	137	:	: :::	:::	:

Db	489	VMAHLSIIQTGNHTHQVPGAPVKG-----PALSIPEFSEWMPMAKMLIYT	536
Qy	138	VQVPADLVQPGQSGVASVDFCFEASLGABGVQWSYTKPRYQKBLMLTQOLPGDNVLLTL	197
Db	537	ILPDGEVI--ADSNFSEIKELCRNKKVDLRPST-SQSLPASQTRLQVITAS-POSGLGLRAV	592
Qy	198	DVSEEQDPSLLYLRLRPVPDALKSLWYKYLCTPQNIITLHNTDLP-----CLCIQV	247
Db	593	DQS-----VLLLKPESE-LSPSWIYMLPGWQ-----QNKFPSSRLSEDEDCILYXS	639
Qy	248	W-----SLEPDSRERVCFPPREDPG--AHRNLMHIARLVLSPGVWOLDAPCC---LPG	296
Db	640	WLAEBKHTNLVPHGTEKQVRYVEDMGLTAFTNLMIKLPILICFDYGNVPISAPRVFEDLAF	699
Qy	297	KVTLICWQAPDQSPCQPLVPPYPQKATWNEPDQFQLVAGHNLCVQVSTWKBVQLQACSW	356
Db	700	TPEISWSLRTLLSKRPREP--PRKDPSSNDPLTETIRKYPETWV----WDIVTVNSIQL	753
Qy	357	A-----DSLGPFKDMLLVEMKTKGLNNTSVCALE	385
Db	754	AREVMTVPDITTEWKAGALCLSNDDTGLGLSSVWPLO	789

RESULT 15

tumor suppressor protein DCC precursor - human
 N:Alternate names: colorectal cancer suppressor DCC
 C:Species: Homo sapiens (man)
 C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
 C:Accession: A54100; A40098
 R:Redick, L.; Cho, K.R.; Fearon, E.R.; Wu, T.C.; Kinzler, K.W.; Vogelstein, B.
 Genes Dev. 8, 1174-1183, 1994
 A:Title: The DCC gene product in cellular differentiation and colorectal tumorigenesis.
 A:Reference number: A54100; MUID:95011532; PMID:7926722
 A:Accession: A54100
 A:Molecule type: mRNA
 A:Residues: 1-1447 <HED>
 A:Cross-references: UNIPROT:P43146; UNIPARC:UPI00000358B3; EMBL:X76132; NID:G453209; PID:G453209; J.M.; Kern, S.E.; Simons, J.W.; Ruppert, J.M.; Hamilt
 R:Pearon, E.R.; Cho, K.R.; Nigro, J.M.; Kern, S.E.; Simons, J.W.; Ruppert, J.M.; Hamilt
 Science 247, 49-56, 1990
 A:Title: Identification of a chromosome 18q gene that is altered in colorectal cancers.
 A:Reference number: A40098; MUID:90100559; PMID:2294591
 A:Accession: A40098
 A:Molecule type: mRNA
 A:Residues: 1-750 <PEA>
 A:Cross-references: UNIPARC:UPI0000016A7D8; GB:M32292; NID:G181492; PID:AAA35751.1; PID:AAA35751.1
 C:Genetics:

[illegible]

Tue Aug 22 11:34:38 2006

```

276 ----- 275
Db 248 NVVAIEGDAVLECCVSGYPPSPFTWLRGEVQLRSKKYSLGGSNLLISNVTTDDSGM 307
QY 276 -----ARLVLSPGVWQDAPCCCLPGKVTLCWQAPD-QSPCQPLVPVP- 318
Db 308 YTCVVYKRNENISASAEITVLVP-PWFLNHPNL-----YAYESMDIEFECTVSGKPVPT 361
QY 319 ---OKNATVNEPQDFQLVAGHENLCVQVSTWEKVQLQACSWADSLGPFKDD---MLIVE 371
Db 362 VNMWKGNDVVPSPDIFQIVGGSNLRI-----LGVKSDGEGFYQCVAE 403
QY 372 MKTGLNNTSVCALEPSGCTP-----LPSMASTRARLGEELLQDFRSHQCMOL 419
Db 404 NEAGNAQTSAQILVFKPAIPSSSVLPAPRDVVPVLSRFRVLS----- 448
QY 420 WNDNNMGSILWACPMCKYIHRRWVLYWLACLLLAALFFELLKKDRRKAARG-S-RTALLL 478
Db 449 -----WRPPAE-----AKGNIQTFTVP 465
QY 479 HSADGAGYERLYGALASALSOMPLR-----VAVDLWSRRELSAHGALAWFHHQ 526
Db 466 FREGDNRERANTTQPGSLQLTGVLKPEAMYTFRVVAYNEMGPGESS----- 514
QY 527 RRRILQEGGVILLFSPAQAQOOWLO-----LQVPEGPHDALAAWLSCVLPDFLO 579
Db 515 -----QPIKVA-TQPELQVPGPVENLQAVSTSTSLITWEP---PAYAN 555
QY 580 GR-----ATCRYGVGYFDGL 594
Db 556 GPVQGYRLFCTEVSTGKEQNIENV DGL 581
```

Search completed: August 16, 2006, 11:46:57
Job time : 48 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2006, 11:37:41 ; Search time 306 Seconds
(without alignments)
2037.453 Million cell updates/sec

Title: US-10-719-202-2

Perfect score: 3605

Sequence: 1 MPVSWFLSLALGRNPFVWS.....SSRPGCCBWDGLPCTTLE 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

! Pred. No. is the number of results predicted by chance to have a
! score greater than or equal to the score of the result being printed,
! and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3605	100.0	674	1	I17RC MOUSE
2	2281	63.3	791	1	I17RC HUMAN
3	1627	45.1	308	2	Q8BP15 MOUSE
4	838.5	23.3	267	2	Q8N2D7 HUMAN
5	350	9.7	637	2	Q6AZ51 RAT
6	338.5	9.4	637	2	Q8BH06 MOUSE
7	310.5	8.6	617	2	Q8K4C1 MOUSE
8	310	8.6	667	2	Q8NRP9 HUMAN
9	309	8.6	551	2	Q8N8H7 HUMAN
10	307.5	8.5	436	2	Q315F0 MOUSE
11	282.5	7.8	591	2	Q6NSU9 MOUSE
12	280.5	7.8	330	2	Q4RJU4 TETNG
13	214	5.9	311	2	Q8R335 MOUSE
14	206.5	5.7	336	2	Q6ZVW7 HUMAN
15	196	5.4	234	2	Q6PTB8 RAT
16	167	4.6	864	1	I17RA MOUSE
17	166	4.6	234	2	Q8C5D0 MOUSE
18	151.5	4.2	866	1	I17RA HUMAN
19	121	3.4	390	2	Q8N8H8 HUMAN
20	121	3.4	2837	2	Q5ZPA6_DELT
21	120	3.3	638	2	Q3QM15_GAMM
22	117	3.2	482	2	Q8TEC2 HUMAN
23	117	3.2	1217	2	Q2NKJ3 HUMAN
24	116.5	3.2	745	1	I17RD BRARE
25	116.5	3.2	1711	1	PTPRV RAT
26	116	3.2	1388	2	Q57UR7 TRYXYP
27	115.5	3.2	794	2	Q4SK16_TETNG
28	115.5	3.2	4905	2	Q4FZJ3 LEIMA
29	115	3.2	772	2	Q4Q1V2 LEIMA
30	114.5	3.2	690	2	Q3R490_XYLFA
31	114.5	3.2	690	2	Q3RD47_XYLFA

32	114.5	3.2	1013	2	O53499 MYCTU
33	114.5	3.2	1013	2	Q7T218 MYCBO
34	114.5	3.2	1217	2	Q5RDX3_PONPY
35	114	3.2	767	2	Q3P288_9GAMM
36	114	3.2	3168	2	Q881Q4_PSESM
37	113	3.1	427	2	Q7PNN1_ANOGA
38	112.5	3.1	1246	2	Q4KAH7_PSEFS
39	112	3.1	2067	2	Q5DOR2_GIBMO
40	111.5	3.1	690	2	Q3R999_XYLFA
41	111	3.1	1181	2	Q4DXU2_TRYCR
42	110.5	3.1	394	2	Q888Z2_PSESM
43	110.5	3.1	698	2	Q87C70_XYLFT
44	110.5	3.1	848	2	Q7WIW4_BORBR
45	110.5	3.1	954	2	Q8VJQ4_MYCTU

ALIGNMENTS

RESULT 1
I17RC MOUSE STANDARD; PRT; 674 AA.
AC Q8K4C2; Q99J43;
DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Interleukin-17 receptor C precursor (IL-17 receptor C) (IL-17RC)
DE (Interleukin-17 receptor-like protein) (IL-17RL).
GN Name=il17rc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Gilbert J.M., Gorman D.M.;
RT "Identification of novel IL-17 related receptors.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC STRAIN=129; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8K4C2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K4C2-2; Sequence=VSP_014142, VSP_014143, VSP_014144;
CC Note=No experimental confirmation available;
CC -----

O53499 mycobacteri
Q7t218 mycobacteri
Q5rdx3 pongo pygma
Q3p288 shewanella
Q881q4 pseudomonas
Q7pnn1 anopheles g
Q4kah7 pseudomonas
Q5d0r2 gibberella
Q3r999 xyella fas
Q4dxu2 trypanosoma
Q888z2 pseudomonas
Q87c70 xyella fas
Q7wiw4 bordetella
Q8vjg4 mycobacteri

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyaama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4), AND VARIANT
RP SER-182.
RC TISSUE=uterus;
EX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PROTEIN SEQUENCE OF 21-35.
EX PubMed-15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RP ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX PubMed-11706037; DOI=10.1074/jbc.M109372200;
RA Haudenschild D., Moseley T., Rose L., Reddi A.H.;
RT "Soluble and transmembrane isoforms of novel interleukin-17 receptor-
RT like protein by RNA splicing and expression in prostate cancer.";
RL J. Biol. Chem. 277:4309-4316(2002).
RN [7]
RP INDUCTION BY HGF AND VEGF.
RX PubMed-14504135; DOI=10.1038/sj.bj.0705494;
RA Gerritsen M.E., Tomlinson J.E., Zlot C., Ziman M., Hwang S.;
RT "Using gene expression profiling to identify the molecular basis of
RT the synergistic actions of hepatocyte growth factor and vascular
RT endothelial growth factor in human endothelial cells.";
RL Br. J. Pharmacol. 140:595-610(2003).
CC CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Soluble isoforms
CC may be produced.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q8NAC3-1; Sequences=Displayed;
CC Note=No experimental confirmation available;
CC

CC Name=2;
CC IsoId=Q8NAC3-2; Sequences=VSP_014138;
CC Name=3;
CC IsoId=Q8NAC3-3; Sequences=VSP_014138, VSP_014139;
CC Note=No experimental confirmation available;
CC Name=4;
CC IsoId=Q8NAC3-4; Sequences=VSP_014138, VSP_014139, VSP_014140,
CC VSP_014141;
CC Note=No experimental confirmation available;
CC TISSUE SPECIFICITY: Expressed in brain, cartilage, colon, heart,
CC intestine, kidney, liver, lung, muscle, placenta, and prostate.
CC Low expression in thymus and leukocytes. Expressed (at protein
CC level) in prostate and prostate cancer, skeletal muscle, kidney
CC and placenta.
CC -I- INDUCTION: By HGF and VEGF.
CC
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
CC EMBL; AF458065; AAM77569.1; -; mRNA.
CC EMBL; AY358840; AA089199.1; -; mRNA.
CC EMBL; AY359098; AA089456.1; -; mRNA.
CC EMBL; AK029207; BAC04001.1; -; mRNA.
CC EMBL; BC006411; AA064111.1; -; mRNA.
CC EMBL; ENSG00000163702; Homo sapiens.
CC HGNC; HGNC:18358; IL17RC.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Membrane; Polymorphism; Receptor; Signal; Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 791 Interleukin-17 receptor C.
FT
FT TOPO DOM 21 538 /FTID=PRO_0000011034.
FT TRANSMEM 539 559 Extracellular (Potential).
FT TOPO DOM 560 791 Potential.
FT CARBOHYD 189 189 Cytoplasmic (Potential).
FT CARBOHYD 257 257 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 420 420 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 443 443 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 477 477 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 36 106 Missing (in isoform 2, isoform 3 and
FT isoform 4).
FT /FTID=VSP_014138.
FT VARSPLIC 264 278 Missing (in isoform 3 and isoform 4).
FT /FTID=VSP_014139.
FT VARSPLIC 579 624 AAAGRAALLYSADDSGFERLVGALCALCOLPLRVAVDL
FT WSRRE -> GEWEQALGGPPGSOACASSPLSPVFSGS
FT GRQGRGSAPLSR (in isoform 4).
FT /FTID=VSP_014140.
FT VARSPLIC 625 791 Missing (in isoform 4).
FT /FTID=VSP_014141.
FT VARIANT 182 182 L -> S (in dbSNP:708567).
FT /FTID=VAR_022680.
FT CONFLICT 241 241 E -> G (in Ref. 2; AAQ89199).
FT SEQUENCE 791 AA; 86294 MW; E0A636BCB472317 CRC64;

Query Match 63.3%; Score 2281; DB 1; Length 791;
Best Local Similarity 58.9%; Pred. No. 4.5e-170;
Matches 458; Conservative 66; Mismatches 134; Indels 120; Gaps 8;

QY 1 MPVSWFLSLALGRNPVVVSRLMEPQDTARCS----- 34
Db 1 MPVSWFLSLALGRSPVLSRLVGPQDATHCSVSLPMEWDERLRVQFLAQOQLSLA 60
QY 35 -----LGLSCHLWDGDLCT 49
Db 61 PVTATARTALSLGSGADRGREERGKSWCLSLGGSGNTEPQKKGUSCRWDSDILCL 120
QY 50 PGSLSQSPGVLVPTRLQTELVLRCPOKTCALRVVVVHLAVHGHWAEPES-----AGKS 105
|| : ||||| || ||||| ||||| : || ||||| ||||| : || :

Db 121 PGDIVPAPGVLPATPHTQTELVLRCQKQETDCDLCLRVAVHLAVHGWEEPEDEKFGGA 180

Qy 106 DSELQESRNALQAOVVLFOAYPIARCALLEVOVADIVQVQSGVSAVFDFCFEASLGA 165

Db 181 DLGVEPRNASLQAOVVLFOAYPIARCALLEVOVADIVQVQSGVSAVFDFCFEASLGA 240

Qy 166 EQVIMSYTKPRYKELNLQQLP-----DGNVLLTLTVSE 201

Db 241 EVRINSYTPRYEKELNHTQQLPDCRGLVWNSIPSCWALPWLNSADGDNVHLVNLVSE 300

Qy 202 EQDFSELYLRPVDPDALKNYKNTLGPQNTLHTDLVPCIQVWLSLEPDSERVEFCP 261

Db 301 EQHFGLSLYNQVQGPQKPRWHLNLTGPQITLHTDLVPCIQVWLSLEPDSERVEFCP 360

Qy 262 FREDPCGHRNLWHIARLVLSPGVWOLDAPCCLPKGVKVLTCQWAPDQSPQPLVPPVPPQKN 321

Db 361 FREDPCGHRNLWHIARLVLSPGVWOLDAPCCLPKGVKVLTCQWAPDQSPQPLVPPVPPQKN 420

Qy 322 ATVNEPQDFOLVAGHPNLCVQVSTWVKVQLQACSWADSLGFFKDDMLLVEMKTLGLNLTSV 381

Db 421 VTVDKVLFFLLKGGHNPCLVQVNSSEKLLQCECLWADSLGFFKDDMLLVEMKTLGLNLTSV 480

Qy 382 CALEPSCGCTPLPSMASTRARLGEELLQDFRSHQCHQWLDNDWNSIWCAPMDKYTHRW 441

Db 481 CALEPSCGCTPLPSMASTRARLGEELLQDFRSHQCHQWLDNDWNSIWCAPMDKYTHRW 539

Qy 442 VLVWLACLLAALFFPFLKDKDRK-----AARGSRATLLHLSADGAGYE 487

Db 540 ALVWLACLLAALFFPFLKDKDRK-----AARGSRATLLHLSADGAGYE 598

Qy 488 RLNGALASALQPLRVAVDLWSRRELSSAHLAWFHQRRLIQEGGVILLFSPAIVA 547

Db 599 RLNGALASALQPLRVAVDLWSRRELSSAHLAWFHQRRLIQEGGVILLFSPAIVA 658

Qy 548 QCQWLQIQVTP-----GPHDALANLWLCVLPDFLQGRATGRYGVYDFGLLHDPDSVSPF 604

Db 659 LCSEWLQGVSGGAGHGFHDAFRASLSCVLPDFLQGRAPGSYVGCDFRLLHDPDAVPLF 718

Qy 605 RVAPFLSLTQPLPAFLDALQGCSTAGRPADRVRYVTOALRSALDSC--TSSEAPG 660

Db 719 RTVPVFTLPSQLPFLGNLQOPRPSRGLQERAEQVSRALQPLDVSFVHPGTPAPG 776

RESULT 3

Q8BP15_MOUSE PRELIMINARY; PRT; 308 AA.

AC Q8BP15_MOUSE, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:110025H02 product:hypothetical protein, full insert sequence.

GN Name=1117c; (Mouse)

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1016/S0076-6879(99)03004-9;

RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning."

RL Methods Enzymol. 303:19-44(1999).

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC PubMed=16141072; DOI=10.1126/science.1112014;

RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,

Ambei-Impimbato A., Apweiler R., Aturaliya R.N., Bailey T.L., Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furum M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwano J., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petkovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Sene S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno K., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;

RT "The transcriptional landscape of the mammalian genome.";

RL Science 309:1559-1563(2005).

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body; DOI=10.1126/science.1112009;

RC PubMed=16141073; DOI=10.1126/science.1112009;

RX RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the PANTOM Consortium;

RT "Antisense transcription in the Mammalian Transcriptome.";

RL Science 309:1564-1566(2005).

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RX Okazaki Y., Furum M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schirml L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).

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RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1038/35055500;
RX MEDLINE=21085660; PubMed=11217851; Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontaiki S.,
RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).

(6)

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1101/gr.145100;
RX MEDLINE=20499374; PubMed=11042159; Sugahara Y., Shibata K., Itoh M.,
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).

(7)

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).

(8)

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurohara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nomazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

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CC

DR EMBL; AK075634; BAC35870.1; -; mRNA.
DR Ensembl; ENSMUSG00000030281; Mus musculus.

DR MGI; MGI:2159336; I117c.
KW Hypothetical protein.

SQ SEQUENCE 308 AA; 33799 MW; 16410BDAACAF666AF CRC64;

Query Match 45.1%; Score 1627; DB 2; Length 308;
Best Local Similarity 99.7%; Pred. No. 3.3e-119;

Matches 307; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 367 MLLVEMTKLTNTSVCALEPSGCTPLPSMASTRARALGERLLQDPRSHQCMLWDDNNG 426

Db 1 MLLVEMTKLTNTSVCALEPSGCTPLPSMASTRARALGERLLQDPRSHQCMLWDDNNG 60

QY 427 SLWACPMNDKYTHRRWLVWTLACILALAFLLKKDRRKAARSRRTALLHLSADGAGY 486

Db 61 SLWACPMNDKYTHRRWLVWTLACILALAFLLKKDRRKAARSRRTALLHLSADGAGY 120

QY 487 ERLVGLASALSOMPLRVAVDLWSRRELSSAGLAWFHQRRLIQEGGVILLFSPAIV 546

Db 121 ERLVGLASALSOMPLRVAVDLWSRRELSSAGLAWFHQRRLIQEGGVILLFSPAIV 180

QY 547 AQCCQWLQQTVEPGPHDAAWLSVLPDFLOGRATGRVGVYFDGLLHSDVSPSPRV 606

Db 181 AQCCQWLQQTVEPGPHDAAWLSVLPDFLOGRATGRVGVYFDGLLHSDVSPSPRV 240

QY 607 APLSLPTLPALFDALQGGCSTAGRPADRVETQALRSALDSCSTSSSAPGCCBWD 666

Db 241 APLSLPTLPALFDALQGGCSTAGRPADRVETQALRSALDSCSTSSSAPGCCBWD 300

QY 667 LGPCTTLE 674

Db 301 LGPCTTLE 308

RESULT 4

ID Q8N2D7_HUMAN PRELIMINARY; PRT; 267 AA.

AC Q8N2D7;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 21-FEB-2006, entry version 9.

DE CDNA PSEC0233 fig, clone HEMBA1006813.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole embryo;

RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,

RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,

RA Nagahari K., Sugano S., Isogai T.;

RT "HRI human cDNA sequencing project";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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CC

DR EMBL; AK075534; BAC11677.1; -; mRNA.

DR Ensembl; ENSG00000163702; Homo sapiens.

SQ SEQUENCE 267 AA; 29696 MW; 490FICE9699D5B2C CRC64;

Query Match 23.3%; Score 838.5; DB 2; Length 267;

Best Local Similarity 61.4%; Pred. No. 2.6e-57;

Matches 172; Conservative 25; Mismatches 56; Indels 27; Gaps 5;

QY 1 MPVSWFLSLALGNRVVVSRLERLWEPDPTARCSLGLSCHLWDGVLCLPGLQAPGPV 60

Db 1 MPVSWFLSLALGNRVVVSRLERLWEPDPTARCSLGLSCHLWDGVLCLPGLQAPGPV 60

QY 61 LVPFELQELVLRCPQKTDCLRVVAVHGHVWAEPEP-AGKSDSELQSRNAS 116

Db 61 LVPFELQELVLRCPQKTDCLRVVAVHGHVWAEPEP-AGKSDSELQSRNAS 120

QY 117 LQAOVWLSFOAYPTIARCALEVQVPAVLVQPGQSVGSVAFDCEASLGAELVQWSTKPR 176

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121 LQAQVLSFQAYPTARCVLLEVQVFAALVQFGSGVGVYDCEFAALGEVWINSYTOPR 180
177 YKELNLTQOLP-----DGDNVLTLVDSEEQDFSLYLRLPVPDALKSLWKYKLT 227
181 YKELNLTQOLPALPWLNVNSADGDNVHLVNLVSEEQHFGLSLVNQVQPPKPRWHKNLV 240
228 GPONITL-NHTDLVPCICIQVWSLEPDSERVFPCFPREDP 266
241 RPPPSVHSHCRMPV-----QRTQ-CHIREDP 267

RESULT 5
Q6AZ51 RAT PRELIMINARY; PRT; 637 AA.
AC Q6AZ51, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 13-SEP-2004, entry version 1.
DE Similar to Interleukin 17 receptor E isoform 1.
GN Name=Il17re;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN RATTUS NORVEGICUS.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN RATTUS NORVEGICUS.
RC TISSUE=Lung;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
[2]
RN RATTUS NORVEGICUS.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigena, and Thymus;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzi R., Shimokawa K.,
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RA Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
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RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,

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RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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RA Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugitara K., Sultana K., Takenaka Y., Taki K.,
RA Tamoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
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RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RT "The transcriptional landscape of the mammalian genome.",
RL Science 309:1559-1563 (2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG Riken Genome Exploration Research Group, and Genome Science Group
RT (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome",
RL Science 309:1564-1566 (2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs",
RL Nature 438:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection",
RL Nature 409:685-690 (2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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RA Kondo S.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
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RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpora quadrigemina, and Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer",
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Adipose, and Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Inamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
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RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RA Li T., Li X., Liu L., Chang Z., Fu X.-Y.,

RT "Identification and Functional Characterization of A Novel Interleukin
 RT 17 Receptor: A Possible Mitogenic Activation Through RAS/Mitogen-
 RT Activated Protein Kinase Signaling Pathway.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 CC
 CC EMBL; AK046302; BAC32678.1; -; mRNA.
 DR EMBL; AK046713; BAC32842.1; -; mRNA.
 DR EMBL; AK169498; BAE41201.1; -; mRNA.
 DR EMBL; DQ092339; AAZ85958.1; -; mRNA.
 DR EMBL; ENSMUSG00000043088; Mus musculus.
 DR MGI; MGI:1889371; I117re.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Hypothetical protein; Receptor.

Query Match 9.4%; Score 338.5; DB 2; Length 637;
 Best Local Similarity 27.5%; Pred. No. 1.6e-17;
 Matches 131; Conservative 56; Mismatches 222; Indels 67; Gaps 18;
 QY 224 KNLTPGQNTITNHTDLVPCLCIQVWSLEPDSERVFCEPPREDPGAH-RNLWHIARLRVLS 282
 DB 183 KIVSGGHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCFQSWPEAYGSDFWQSIKFTDYS 242
 QY 283 PG---VWQLDAPCCLPCKVTLCQAPDQSPQCPPLVPPVPOKNAVNEPQDFQLVAG---H 336
 DB 243 QHNQVMWALTLCPLKLEASLCWRQDPLTPCETL-----PNATAQSEGWYLENVLDLH 296
 QY 337 PNLGVQVSTWEKVLQALC-----SWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSG 388
 DB 297 PQLCFKFS-FENSSHVECPHQSGSLPSTWTSMDT-QAQLTLHFSSRTYATFSAWSDPG 354
 QY 389 C---TPLPSMASTRAARLGEELLQD-----FRSHQCMQVNDNDNMGSLW---ACPMDKYI 437
 DB 355 LGPDTMPVPVYSISQTOGSPVTLDLIIPFLRQNCILVWRSQ-VHFAWKVLCF---DVS 411
 QY 438 HRRVWVWLACLLAAALFFLLKKORRKAARG-SRTALLHSDAGAGYERLVGALASA 496
 DB 412 HRHGLLILALLATLVGVVLLGRLLPGSGRTPLVLLHAAADSEARLLVGAALAE 471
 QY 497 LSQM---PLRVAVDLWSRRELSAHGALAWFHRRRILOEGGVVILLFSPAQAQCCQWL 553
 DB 472 LRTALGGGRDVIQVDMEGTHVARIGPLPWLWAARVAREQGVVLLWNCAGPS-----525
 QY 554 QLQVTEPGPHDALAAWLSVLPDQGRATGRYGVYVDFGLLHPDSVPSPFRVAPLPSLP 613
 DB 526 ---TACSGDPQAASLTLLCAAPRL-----LLAYFSRLCAKGDIPRLRALPRVRL 575
 QY 614 TQLPAFLDALOGGCTSA-----GRPADRVERVTOA-----LRSALDCTSSSEAP 659
 DB 576 RDLPRLLRALDAQPATLASSWSHLGAKRCLKNRLEQCHLLEAKDDYQGSTNSP 631

RESULT 7
 ID Q8K4C1 MOUSE PRELIMINARY; PRT; 617 AA.
 AC Q8K4C1;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE IL-17RE.
 GN Name=Il17re;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP Gilbert J.M., Gorman D.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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 CC
 CC EMBL; AF458068; AAM77572.1; -; mRNA.
 DR EMBL; ENSMUSG00000043088; Mus musculus.
 DR MGI; MGI:1889371; I117re.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Hypothetical protein; Receptor.
 Query Match 8.6%; Score 310.5; DB 2; Length 617;
 Best Local Similarity 25.7%; Pred. No. 2.4e-15;
 Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;
 QY 224 KNLTPGQNTITNHTDLVPCLCIQVWSLEPDSERVFCEPPREDPGAH-RNLWHIARLRVLS 282
 DB 183 KIVSGGHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCFQSWPEAYGSDFWQSIKFTDYS 242
 QY 283 PG---VWQLDAPCCLPCKVTLCQAPDQSPQCPPLVPPVPOKNAVNEPQDFQLVAG---H 336
 DB 243 QHNQVMWALTLCPLKLEASLCWRQDPLTPCETL-----PNATAQSEGWYLENVLDLH 296
 QY 337 PNLGVQVSTWEKVLQALC-----SWADSLGPFKDDMLLVEMKTLGNNTSVCALEPSG 388
 DB 297 PQLCFKFS-FENSSHVECPHQSGSLPSTWTSMDT-QAQLTLHFSSRTYATFSAWSDPG 354
 QY 389 C---TPLPSMASTRAARLGEELLQD-----FRSHQCMQVNDNDNMGSLW---ACPMDKYI 437
 DB 355 LGPDTMPVPVYSISQTOGSPVTLDLIIPFLRQNCILVWRSQ-VHFAWKVLCF---DVS 411
 QY 441 WVLV-----WVACLLAAALFFLLKKORRKAARG-SRTALLHSDAGAGYERLVGAL 493
 DB 402 WKHVLCPDAPYPTQLLL-----RSLGSGRTPLVLLHAAADSEARLLVGAAL 448
 QY 494 ASALSQM---PLRVAVDLWSRRELSAHGALAWFHRRRILOEGGVVILLFSPAQAQCCQ 550
 DB 449 AELLRTALGGGRDVIQVDMEGTHVARIGPLPWLWAARVAREQGVVLLWNCAGPS---505
 QY 551 QWLQLOQVTEPGPHDALAAWLSVLPDQGRATGRYGVYVDFGLLHPDSVPSPFRVAPL 610
 DB 506 ---TACSGDPQAASLTLLCAAPRL-----LLAYFSRLCAKGDIPRLRALPR 552
 QY 611 SLPTQLPAFLDALOGGCTSA-----GRPADRVERVTOA-----LRSALDCTSSSEAP 659
 DB 553 RLLRDLPRLLRALDAQPATLASSWSHLGAKRCLKNRLEQCHLLEAKDDYQGSTNSP 611

RESULT 8
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 AC Q8NFR9;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE IL-17RE (GSSR3056).
 GN Name=Il17re; ORFNames=UNQ3056;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP Gilbert J.M., Gorman D.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RESULT 9
 ID Q8NFR9 HUMAN PRELIMINARY; PRT; 667 AA.
 AC Q8NFR9;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE IL-17RE (GSSR3056).
 GN Name=Il17re; ORFNames=UNQ3056;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP Gilbert J.M., Gorman D.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RESULT 10
 ID Q8NFR9 HUMAN PRELIMINARY; PRT; 667 AA.
 AC Q8NFR9;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE IL-17RE (GSSR3056).
 GN Name=Il17re; ORFNames=UNQ3056;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP Gilbert J.M., Gorman D.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.


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Db 430 LGGGRDVIIVDLMEGTHVARIGPLWLAARERAREQGTVLLWNCAGPS-----TA 481
Qy 558 VERPGHDAALWLCVLPDFLQGRATGRVGVYFGLLHPDSVPSPFRVAPLFLSLPTQLP 617
Db 482 CSGDQPMASRLTLCAAPRL-----LLAYFSLCAKGDIPRLALPRYLLRLDLP 533
Qy 618 AFLDALOGGCSFSA-----GRPADRVERVTOA-----LRSALDSCTSSEAP 659
Db 534 RLRLALDAQPATLASSWSHLGAKRCLKNRLEQCHLLELEAAKDYQGSTNSP 585

RESULT 12
QARJ04 TETNG
ID QARJ04 TETNG PRELIMINARY; PRT; 330 AA.
AC QARJ04;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome 9 SCAP15033, whole genome shotgun sequence.
GN ORFNames=GSTENG00033274001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15496914; DOI=10.1038/nature03025;
RX Expression driven by an MMTV-LTR enhancer; STRAIN=C2EHC II;
RA Jallou O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costat C., Bernot A.,
RA Nicaud S., Jarfe D., Fisher S., Lutfalla G., Doessat C., Segurens B.,
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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAAB01015033; CAG11338.1; -; Genomic DNA.
SQ SEQUENCE 330 AA; 36170 MW; 1D189B0B715289D2 CRC64;

Query Match 7.8%; Score 280.5; DB 2; Length 330;
Best Local Similarity 29.8%; Pred. No. 2.4e-13;
Matches 89; Conservative 36; Mismatches 103; Indels 71; Gaps 12;

Qy 431 CPMDKYIHRRWVLMVLAALLAALF--PFL-----LILKDRKKAAGSR 473
Db 19 CP----PASSRW--RWSLLFTGVLLFLFFLGAYFIQALGYMWRWKEDDLKGVGGS 73
Qy 474 TALLHSADG-AGYERLVGALASALSQMLPRVAVDLMSRRLSAGHALWFHQRRLQ 532
Db 74 QAVLLYPPDGPALPKLNNRGLSILRTGLFTVSLDLSQGLSALGPVPLHSLRNQVR 133
Qy 533 EGGVILLFSPAQAQCOQW-----LQ-----LQTPGPHDALAAILSCVLP 577
Db 134 HGGKVLLVLTQATWLRAEENGAQSWERKVASLEKNKVMDTVSPASSDVFATSLSCVLADH 193

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Qy 578 LQGRATGRVGVYFGLLHPDSVPSPFRVAP-----LFSLPQLPAFLDALOGG---C 627
Db 194 LQGRAGERFMLVQFESL--PPKPGGFRPLPFCGLHVLSPQSGLFELTAGAGPVS 251
Qy 628 STSAGRPADRVVTOA-----LRSALDSCTSSEAPGCCSEWDLGP 669
Db 252 NASARRRRRAGVLRMASRFLARGLSGSLTGTLLHIRTTSQSCMGD---GVEDSWETMP 306

RESULT 13
Q3R335 MOUSE
ID Q3R335 MOUSE PRELIMINARY; PRT; 311 AA.
AC Q3R335;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE I117re protein.
GN Name=I117re;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer; STRAIN=C2EHC II;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2EHC II; TISSUE=Mammary tumor metastasized to lung.
RC MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC026737; AAH26737.1; -; mRNA.
DR Ensembl; ENSMUSG0000043088; Mus musculus.
DR MGI; MGI:1889371; I117re.
SQ SEQUENCE 311 AA; 34103 MW; 00E706D6617CFF15 CRC64;

Query Match 5.9%; Score 214; DB 2; Length 311;
Best Local Similarity 27.0%; Pred. No. 3.8e-08;
Matches 89; Conservative 32; Mismatches 141; Indels 68; Gaps 12;

Qy 353 ACSWAD-SLGFPRKDDMLLVEMKTLNNTSVCALEPSCGCTPLPSMASTRARLGBELLOD- 410
Db 21 SAAMSDPGLGP-----DTMPPPVVISQTQSGSVFVMDL 54
Qy 411 ----FRSHQCQMLWNNDDNGLSW---ACPMDKYIHRRWVLMVLAALLAALFFFLILKK 463

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Qy	490	VGALASALSON---	PLRVAVDLWSRREL	SAHGALAWFHQRRRI	LOEGGVILLFSPA	AV	546		
Db	62	VGALAEELLR	TALGGGRD	VIVDLWEGTH	VARIGPLFWLWA	ARERVAR	EQGTVILLWSCAGP	121	
Qy	547	AQCOOMLO	QOTVEB	PGHDALA	AWLSCVLP	DFLOGRAT	GRYGVY	PDGLLHPDSVPSERV	606
Db	122	S-----	TACSGDP	POTASL	RTLSCA	APRQL-----	LLAYFS	RLCAKGDIPGLRA	165
Qy	607	APLPSLPT	QLPAP	LDALQCG	CGST	SAGRPAD	RVER-----	VTQALRSALDSC	652
Db	166	LPRYRLRD	LPRLRALD	-----	ARPATL	ATSN	SHLGAKE	CKSRLELC	209

Search completed: August 16, 2006, 11:46:08
Job time : 311 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2006, 11:46:22 ; Search time 52 Seconds
(without alignments)
1134.532 Million cell updates/sec

Title: US-10-719-202-2
Perfect score: 3605
Sequence: 1 MEVSWFLSLALGRNPVVVS.....SSEAPGCCSEWDLGPCTTLE 674

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:**
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:**
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:**
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:**
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCFUS_COMB.pep:**
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RG_COMB.pep:**
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2339	64.9	705	2	US-09-747-259-14
2	2339	64.9	705	2	US-09-816-744-14
3	2281	63.3	791	2	US-10-104-047-3296
4	310.5	8.6	617	2	US-09-188-930-303
5	310.5	8.6	617	2	US-09-312-283C-303
6	310	8.6	667	2	US-09-747-259-16
7	310	8.6	667	2	US-09-816-744-16
8	193.5	5.4	226	2	US-09-893-737-328
9	167	4.6	864	1	US-08-620-694A-2
10	167	4.6	864	2	US-09-022-255-2
11	167	4.6	864	2	US-09-022-696-2
12	167	4.6	864	2	US-08-978-773-2
13	167	4.6	864	2	US-09-022-253-2
14	167	4.6	864	2	US-09-022-260-2
15	167	4.6	864	2	US-09-022-259-2
16	167	4.6	864	2	US-09-022-257-2
17	167	4.6	864	2	US-09-549-679-2
18	167	4.6	864	2	US-09-488-728-2
19	151.5	4.2	866	1	US-08-620-694A-10
20	151.5	4.2	866	2	US-09-022-255-10
21	151.5	4.2	866	2	US-09-022-696-10
22	151.5	4.2	866	2	US-08-978-773-4
23	151.5	4.2	866	2	US-09-022-253-10
24	151.5	4.2	866	2	US-09-022-260-10
25	151.5	4.2	866	2	US-09-022-259-10
26	151.5	4.2	866	2	US-09-022-257-10

Sequence 10, Appl
Sequence 1, Appl
Sequence 403, App
Sequence 4, Appl
Sequence 412, App
Sequence 125, App
Sequence 2263, App
Sequence 214, App
Sequence 2, Appl
Sequence 8253, Ap
Sequence 2, Appl
Sequence 18, Appl
Sequence 6842, A
Sequence 10063, A
Sequence 10064, A
Sequence 20327, A
Sequence 28, Appl
Sequence 28, Appl

27 151.5 4.2 866 2 US-09-549-679-10
28 151.5 4.2 866 2 US-10-033-522-1
29 151.5 4.2 866 2 US-09-949-002-403
30 151.5 4.2 866 3 US-09-488-728-4
31 149.5 4.1 876 2 US-09-949-002-412
32 149 4.1 330 2 US-09-188-930-125
33 149 4.1 330 2 US-09-312-283C-125
34 116 3.2 1217 2 US-10-104-047-2263
35 114.5 3.2 1013 2 US-09-712-363-214
36 114.5 3.2 1711 1 US-08-342-930-2
37 110 3.1 686 2 US-09-543-681A-8253
38 107 3.0 986 2 US-08-311-731A-2
39 105.5 2.9 1457 2 US-09-713-273A-18
40 104.5 2.9 1237 2 US-09-949-016-6842
41 104.5 2.9 1239 2 US-09-949-016-10063
42 104.5 2.9 1239 2 US-09-949-016-10064
43 103 2.9 921 2 US-09-252-991A-20327
44 102.5 2.8 1498 1 US-08-404-531B-28
45 102.5 2.8 1498 2 US-08-476-900A-28

ALIGNMENTS

RESULT 1
US-09-747-259-14
; Sequence 14, Application US/09747259
; Patent No. 6569645

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: VanLookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381C1P1(US)

CURRENT APPLICATION NUMBER: US/09/747,259

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: US 09/311,832

PRIOR FILING DATE: 1993-05-14

PRIOR APPLICATION NUMBER: US 60/172,096

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: PCT/US99/31274

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: US 60/175,481

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/US00/04341

PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 60/191,007

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/07532

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/15264

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: US 60/213,087

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: US 09/644,848

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: PCT/US00/23328

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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-14

Query Match      64.9%; Score 2339; DB 2; Length 705;
Best Local Similarity 66.3%; Pred. No. 1.4e-244;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

QY 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVDVLCPLGSLQAPGV 60
Db 1 MPVSWFLSLALGRSPVVLSERLVGPQDATHCSPLSCRLWDSILCLPGDIVPAPGV 60

QY 61 LVPTLQTELVLRCQKTDCLARVVRVVHVLAVHGWABPEE-----AGKSDSELQSRNAS 116
Db 61 LAPTHLQTELVLRCQKTDCLCLRVAVHLAVHGWABPEE-----AGKSDSELQSRNAS 120

QY 117 LQAOVVLFOAYPIARCALLEVQVPADLVQPCQSVGSVAVDFCFEASLGAEOIWSYTKPR 176
Db 121 LQAOVVLFOAYPIARCALLEVQVPADLVQPCQSVGSVAVDFCFEASLGAEOIWSYTKPR 180

QY 177 YQKELNLTQQLP-----DGDNVLLTLDVSEEDQSFLLYLRLPVPDALKSLWYKNLT 227
Db 181 YKELNHTQQLPALPWLNVSDGDNVHLVNLVSEEQHFGLSLYWNVQVQPPKPRMHKNLT 240

QY 228 GPQNTITLHNTDLVPCLCIQVWSLEPDSERVECPFPREDPRAHNLWHIARLVLSPGVWQ 287
Db 241 GPQITITLHNTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHNLWQAARLLTLQSWL 300

QY 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWE 347
Db 301 LDAPCCLPAAALCWRAPEGDPCCQPLVPPLSWENVTVDKVLEFPLKLGHPNLCVQVNSSE 360

QY 348 KVQLQACSWADSLGPFKDDMLIVEMKTLGNNTSVCALEPSCGCTPLPSMASTRARLGEEL 407
Db 361 KLQLECLWADSLGPKDDVLLLETRGPQDNRSCLALEPSCGCTSLPSKASTRAARLGEYL 420

QY 408 LQDFRSHQCMQLWNNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALFFLLKKDRRK 467
Db 421 LQDLQSGQCLQLW-DDDLGALWACPMCKYIHKRWLVWLACLLFAALSLILLKKDHAK 479

QY 468 -----AARGSRRTALLHSADGAGYERLVGALASALQMPLRVAVDLWSRRE 513
Db 480 GWRLLLKQDVRSGAARG-RAALLIYSADDSGFELVGLASALCQLPLRVAVDLWSRRE 538

QY 514 LSAHGALAFHFFHRRRILOEGGVVILLFSPAAVAQCOQWLQOTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFWFAHQRRQTLQEGGVVILLFSPGVALCSEWLQDGVSGPGAGHPHDAFRASL 598

QY 571 SCVLDPDFLOGRATGRVGVYFGILLHPDSVPFRVAPLFSIPTOLPAFLDALQGCSTNS 630
Db 599 SCVLDPDFLOGRAPGSYGVGACFDRLLHPDAVPALFTVPVFTPLPSQLDFLQALQOPRAPR 658

QY 631 AGRPADRVERTQALRSALDSC--TSSSEAPG 660
Db 659 SGRLQERAEQVSRALQPALDSYFHPGTPAG 690

RESULT 2
US-09-816-744-14
; Sequence 14, Application US/09816744
; Patent No. 6579520
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RESULT 5
US-09-312-283C-303
Sequence 303, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.101LC2
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 617
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-303

Query Match 8.6%; Score 310.5; DB 2; Length 617;
Best Local Similarity 25.7%; Pred. No. 4.6e-24;
Matches 123; Conservative 55; Mismatches 208; Indels 93; Gaps 17;

QY 224 KNLGPGQNTLTHNTDLPCLCIQVMSLEPDSERVEFCPPREDPGAH-RNLWHIARLVLS 282
DB 183 KIVSGGHTVDFEYFLLPCWCIASVLOEDTVRRKKCPQSWPEAYGSDFWQSIRFTDYS 242

QY 283 PG---VWQLDAPCCLPKVTLCWQAPDQSPQPLVPPVQKATVNEPQDFOLVAG--H 336
DB 243 QHNMVMALTLRCPLKLEASLCWRQDPLTPCETL-----PNATAQSEGWILENVDLH 296

QY 337 PNLGVQVSTWVKVQLQAC-----SWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSC 388
DB 297 PQLCPKFS-FENSSHVECPHQSGSLPSWTVMST-DAQOQLTLHFSSRTYATFSAAWSDFG 354

QY 389 C---TPLPSMASTRARLGEELLQD-----FRSHQCMQWLNDDNMGLWACPMCKYIHR 440
DB 355 LGPDTPMPFVYSIQSGSVFVTDLIIFLQENCLVWRS------VHFA 401

QY 441 WVLV-----WLACLLIAALFFLLKKRKAARGSRRTALLHSADGAGYERLVGAL 493
DB 402 WKVLCDDAPYPTQLLL-----RSLGSGRTRPVLLHAAADSEAQRRLVGL 448

QY 494 ASALSOM---PLRVAVDLWSRRRLSAHALAWTHHRRILQEGGVVILLFSAVAQCQ 550
DB 449 AELLRTALGGGRDVIYDLMEGTHVARIGPLPWLWAARERVAREQGTVLLLNACGFS--- 505

QY 551 QNLQLQTVFPGPHDALAAWLSVLPDPLQGRATGRVGVYFDGLLHPDPSVPSFPRVAPLF 610
DB 506 -----TACSGDPOAASLURLLCAAPRL-----LLAYFSRLCAKGDIPRLRALPRY 552

QY 611 SLPTQLPAFLDALQGGCS TSA-----GRPADRVVTOA-----LRSALDSCSSSEAP 659
DB 553 RLLRDLPRLLRALDAQPATLASSWSHLGAKRCLKNRLEQCHLLEAAKDDYQGSTNSP 611

RESULT 6
US-09-747-259-16
Sequence 16, Application US/09747259
Patent No. 6569645
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: VanLookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: PL381R1C1P1(US)
CURRENT APPLICATION NUMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 16
LENGTH: 667
TYPE: PRT
ORGANISM: Homo Sapien
US-09-747-259-16

Query Match 8.6%; Score 310; DB 2; Length 667;
Best Local Similarity 28.1%; Pred. No. 5.9e-24;
Matches 130; Conservative 56; Mismatches 214; Indels 62; Gaps 18;

QY 224 KNLGPGQNTLTHNTDLPCLCIQVMSLEPDSERVEFCPPREDPGAH-RNLW---HTARLR 279
DB 223 KIVSGGHTVELPYEFLLPCLCIEASVLOEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYS 282

QY 280 VLSPGVWQLDAPCCLPKVTLCWQAPDQSPQPLVPPVQKATVNEPQDF---QLVAGH 336
DB 283 QHTQVMVMTLRCPLKLEAALCORHDWHTLCKDL-----FNATARESOGWVLEKVDLH 336

QY 337 PNLGVQVSTWVKVQLQAC-----CSWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSC 389
DB 337 PQLCFKFSFQNSHVECPHOTGSLTSWNVSMST-DAQOQLLHFSRRHATFSAAWSLPG 395

QY 390 ---TPLPSMASTRARLGEELLQD-----FRSHQCMQWLNDDNMGLW---ACPMCKYIH 438
DB 396 QDITLVPVTVTSQARGSSPVSLDLIIFLRPGCCVLMWRS-VQFAWGLLCPDVSYRH 454

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-2

Query Match 4.6%; Score 167; DB 1; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTPSPKNIYINLSVSTQHGELVPLHVE-WTLQTDASILYLEGAELSVLQLTNTER 256
DB 66 KNLTPSPKNIYINLSVSTQHGELVPLHVE-WTLQTDASILYLEGAELSVLQLTNTER 124

QY 257 --VEFCFREDPGAHRLNWHIARLR-VLSPG-----VWOLDAPCCLPKGKVTLCQWAPDQ 307
DB 125 LCVKFP-QFLSMLQHRRKRWRFSFHFVVDQGEYEVTVHHLPKP-----IPDG 171

QY 308 SPCQP-----LVPPVPQKNATVNEPQDFQLVAGHNLGVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVDCEDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230

QY 364 KDDMLLVEMKTLGNTSV-----HTDLVPCLCIQVSWLEPD-----SER 256
DB 231 Q---VLLSEFSDSENHSCFDVYKQIPAPROBEFHQRANVTFTLSKFHWCHHHVQVQPF 287

QY 387 SGC-----TPLESMASRAARLGEELLQDFRSHQCQLWDDNMGSLWACPMCKY 436
DB 288 SSCUNDCLRHATVPCPVISNTTVPK-----PVADY 318

QY 437 IHRWV--LVWLACLLAALFFEL-----LLKDRRKAAGS----- 472
DB 319 I-PLWVGLITLIALLVGSVILVLCMTWRLSGADQEKHGDSDSKINGILPVADLTTPPL 377

QY 473 --RTALLSHADGAGYERLVGALASAL-SQPLVAVDLMSRRRLSAHALAWFHQRRR 529
DB 378 RPRKVIWIVYSDHPLLYVEVWLKFAQLITACGTVEALDLEEQVISEVGMVTWSRQKE 437

QY 530 ILQEGGVVILLFS-----PAAVACCOOVLQTVPEPGPHDALAAWLSVL 574
DB 438 MVENSKIIILCSRGTKQAKWAILGWAEPVQLRCDHW-----KPA-GDLFTAMNWL 490

QY 575 PDFLQGRATGRVGYDFGLLHPDSVPSFPRVAPLFSL 612
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QY 437 IHRRW--LWMLACILLAAALFFFL-----LLKDRKKAARGS----- 472
DB 319 I-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SOMPLRVAVDLWSRRELSAHCALAWFHQR 529
DB 378 RPRKVIWISADHPLYVEVLKFAQLITACGTEVALDLEEQVISEVGVMTWVSQRQOE 437
QY 530 ILQEGGVILLFS-----PAAVAQCOOQLQCTVBPFGPHDAAALWLSCVL 574
DB 438 MVESNSKIILCSRGTOAKKAILGWAEPVQLRCDHW-----KPA-GDLFTAAANNIL 490
QY 575 PDFLQGRATRGVGVYFDGLLHPDSVPSPFRVAPLFSL 612
DB 491 PDFKRPACFGTVVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 11

US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-022-696-2
Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;
QY 224 KNTT--GPQNITLN-----HTDLVPCLCIQVWSLEBD-----SER 256
DB 66 KNTLPSSPKNIYINLSVSTQHGLVPVLHVE-WTLQTDASILYLEGAEISVLQNTN 124

QY 257 --VEFCPFREDPAHRNLWHIARLR-VLSPG-----VMOLDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKP-QELSMQLQHRKRWRFSFSHFVVDPGQGEYEVTVHHLKP-----IPDG 171
QY 308 SPCQP-----LVPVPQKNATVNEPQDFQLVAGHPNLVCYQVSTWEKVLQACSWADSLGPF 363
DB 172 DPNHKSIIFFVDPDCDSKMKMTTSCVSSGSLWDPNITVETLDTQHLRVDPFTLWNEST-PY 230
QY 364 KDDMLLVEMKTKLNTSV-----CA-----LEP-- 386
DB 231 Q---VLLSFSFSEHNSCFDVVVKQIPAPRQEBFHQRANVTFTLSKFHWCHHHVQVOPFF 287
QY 387 SGC-----TPLPSMASTRARALGELQLDFRSHQCMQLWDDNMGSLWACPMWKY 436
DB 288 SSCINDCLRHAVTVPCPVISNTVPK-----PVADY 318
QY 437 IHRRW--LWMLACILLAAALFFFL-----LLKDRKKAARGS----- 472
DB 319 I-PLWVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SOMPLRVAVDLWSRRELSAHCALAWFHQR 529
DB 378 RPRKVIWISADHPLYVEVLKFAQLITACGTEVALDLEEQVISEVGVMTWVSQRQOE 437
QY 530 ILQEGGVILLFS-----PAAVAQCOOQLQCTVBPFGPHDAAALWLSCVL 574
DB 438 MVESNSKIILCSRGTOAKKAILGWAEPVQLRCDHW-----KPA-GDLFTAAANNIL 490
QY 575 PDFLQGRATRGVGVYFDGLLHPDSVPSPFRVAPLFSL 612
DB 491 PDFKRPACFGTVVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 12

US-08-978-773-2
; Sequence 2, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-773-2

Query Match      4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTPCLCICQVMSLEPD-----HTDLVPCLCICQVMSLEPD-----SER 256
Db 66 KNLTPSSPKNIYINLSVSTQHGELVPVLHYE-WTLQTDASILYLEGAELSVLQNTNER 124
QY 257 --VEFCFPREDPGAHNLWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
Db 125 LCVKFP-QFLSLMLOHRRKWRFSFHFVVDPOQEYVTVHLPKP-----IPDG 171
QY 308 SPCQP-----LVPPVPQKNATVNEPQDFQLVAGHNLVCQVSTWEKVOQACSWADSLGPF 363
Db 172 DPNHKSIIIFVDCEDSKMKWTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KDDMLLVEMKTLGNNTSV-----CA-----LEP-- 386
Db 231 Q---VLESFSDSENHSCFVVVKQIFAPRQBEFHQRANVTFTLSKFHWCCHHHVQVQPF 287
QY 387 SGC-----TPLPSTMASTRARLGEELLQDFRSHQCMQLWDDNMGSLWACPMCKY 436
Db 288 SSCLNDCLRHATVPCPVISNTVTPK-----PVADY 318
QY 437 IHRRWV--LVMLACILLLAAALFFFL-----LLKDRRKAARGS-----472
Db 319 I-PLWVYGLITLAILLVGSVIVLIICTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SQMLRVAVDLWSRRELSTAGALAWFHQR 529
Db 378 RPRKVMIVYSADHPLYVEVLKFAQLITACGTEVALDLLEEQVISEVGMVTWVSROKQE 437
QY 530 ILQEGGVVILFS-----PAAVACQOQMLQOTVEPFGPHDALAALWLSCVL 574
Db 438 MVESNSKIIILCSRGTQAKWAILGWAEPAVQLRCDHW-----KPA-GDLFTAAMNML 490
QY 575 PDFLQGRATGRYGVYFDGLLHPDSVPSPFRVAPLFSL 612
Db 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 13
US-09-022-253-2
; Sequence 2, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/022,253
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694

; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-2

Query Match      4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLTPCLCICQVMSLEPD-----HTDLVPCLCICQVMSLEPD-----SER 256
Db 66 KNLTPSSPKNIYINLSVSTQHGELVPVLHYE-WTLQTDASILYLEGAELSVLQNTNER 124
QY 257 --VEFCFPREDPGAHNLWHIARLR-VLSPG-----VWQLDAPCCLPKVTLCWQAPDQ 307
Db 125 LCVKFP-QFLSLMLOHRRKWRFSFHFVVDPOQEYVTVHLPKP-----IPDG 171
QY 308 SPCQP-----LVPPVPQKNATVNEPQDFQLVAGHNLVCQVSTWEKVOQACSWADSLGPF 363
Db 172 DPNHKSIIIFVDCEDSKMKWTTSCVSSGSLWDPNITVETLDTQHLRVDFTLWNEST-PY 230
QY 364 KDDMLLVEMKTLGNNTSV-----CA-----LEP-- 386
Db 231 Q---VLESFSDSENHSCFVVVKQIFAPRQBEFHQRANVTFTLSKFHWCCHHHVQVQPF 287
QY 387 SGC-----TPLPSTMASTRARLGEELLQDFRSHQCMQLWDDNMGSLWACPMCKY 436
Db 288 SSCLNDCLRHATVPCPVISNTVTPK-----PVADY 318
QY 437 IHRRWV--LVMLACILLLAAALFFFL-----LLKDRRKAARGS-----472
Db 319 I-PLWVYGLITLAILLVGSVIVLIICTWRLSGADQEKHGDDSKINGILPVADLTTPPL 377
QY 473 --RTALLHSADGAGYERLVGALASAL--SQMLRVAVDLWSRRELSTAGALAWFHQR 529
Db 378 RPRKVMIVYSADHPLYVEVLKFAQLITACGTEVALDLLEEQVISEVGMVTWVSROKQE 437
QY 530 ILQEGGVVILFS-----PAAVACQOQMLQOTVEPFGPHDALAALWLSCVL 574
Db 438 MVESNSKIIILCSRGTQAKWAILGWAEPAVQLRCDHW-----KPA-GDLFTAAMNML 490
QY 575 PDFLQGRATGRYGVYFDGLLHPDSVPSPFRVAPLFSL 612
Db 491 PDFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPL 528

RESULT 14
US-09-022-260-2
; Sequence 2, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
```



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; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-260-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLIT--GPNITL-----HTDLVPCLCIQVMSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGSLVPLVHVE-WTLQTDASILYLEGAELSVLQNTNER 124

QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKF-QFLSNLQHRRKWRPFSFHFVDPQGEYEVTVHLLPKP-----IPDG 171

QY 308 SPQOP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDCSKMKMTTSCVSSGSLWDPNITVTETLDTQHLRVDFTLWNEST-PY 230

QY 364 KDDMLLVEMTKGLNNTSV-----CA-----LSP-- 386
DB 231 Q-----VLLSEFSDSNHSCFDDVVVKQIFAPROBEFHORANVTTLTKFHWCHHHVQVQPF 287

QY 387 SGC-----TPLEFSMASTRALRGEILLQDFRSHQCQLWDDNMGSLMACPMCKY 436
DB 288 SSCNLDCRLRAVTVPCFVINSITVPK-----PVADY 318

QY 437 IHRRW--LWVLAACLLAALFPFL-----LLKORRKAARGS----- 472
DB 319 I-PLWVYGLTILAILLVGVSIVLIICTWRLSGADQKGGDSKINGILPVADLTTPPL 377

QY 473 --RTALLHSGADGVERLYCALASAL--SQMPLRVAVDLMSRRLSAHGALEWHQRRR 529
DB 378 RPRKRWIVISADHPLYVEVVLKFAQLITACGTEVALDLLEEQVISEVGMVTWYSRQKE 437

QY 530 ILQEGGVVILLFS-----PAAVAQCQQLQLQTVPEPGPHDALAAWLSCVL 574

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-259-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLIT--GPNITL-----HTDLVPCLCIQVMSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGSLVPLVHVE-WTLQTDASILYLEGAELSVLQNTNER 124

QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKF-QFLSNLQHRRKWRPFSFHFVDPQGEYEVTVHLLPKP-----IPDG 171

QY 308 SPQOP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDCSKMKMTTSCVSSGSLWDPNITVTETLDTQHLRVDFTLWNEST-PY 230

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
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; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-259-2

Query Match 4.6%; Score 167; DB 2; Length 864;
Best Local Similarity 20.3%; Pred. No. 3.3e-08;
Matches 105; Conservative 62; Mismatches 167; Indels 184; Gaps 25;

QY 224 KNLIT--GPNITL-----HTDLVPCLCIQVMSLEPD-----SER 256
DB 66 KNLTPSPKNIYINLSVSTQHGSLVPLVHVE-WTLQTDASILYLEGAELSVLQNTNER 124

QY 257 --VEFCFPREDPGAHRLNWHIARLR-VLSPG-----VWQLDAPCCLPGKVTLCWQAPDQ 307
DB 125 LCVKF-QFLSNLQHRRKWRPFSFHFVDPQGEYEVTVHLLPKP-----IPDG 171

QY 308 SPQOP-----LVPPVPQKNATVNEPQDFQLVAGHPNLCVQVSTWKEVKVQLQACSWADSLGPF 363
DB 172 DPNHKSIIIFVPCDCSKMKMTTSCVSSGSLWDPNITVTETLDTQHLRVDFTLWNEST-PY 230
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 16, 2006, 11:48:07 ; Search time 35 Seconds
(without alignments)
1304.753 Million cell updates/sec

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Perfect score: 3605
Sequence: 1 MPVSFWLLSLALGRNPVVVS.....SSEAPGCCENWDLGCTTLE 674

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 243793 seqs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2339	64.9	705	7	US-11-311-555-14
3	2339	64.9	705	7	US-11-311-561-14
4	2339	64.9	705	7	US-11-101-316-162
5	2339	64.9	705	7	US-11-311-554-14
6	2339	64.9	705	7	US-11-376-673-162
7	1086	30.1	343	7	US-11-293-697-2756
8	739	20.5	261	7	US-11-293-697-3960
9	338.5	9.4	637	7	US-11-253-200-14
10	337.5	9.4	661	7	US-11-253-200-111
11	313.5	8.7	609	7	US-11-253-200-8
12	310	8.6	589	7	US-11-253-200-5
13	310	8.6	627	7	US-11-253-200-21
14	310	8.6	650	7	US-11-253-200-107
15	310	8.6	667	7	US-11-311-555-16
16	310	8.6	667	7	US-11-311-561-16
17	310	8.6	667	7	US-11-311-554-16
18	310	8.6	667	7	US-11-253-200-2
19	309	8.6	551	7	US-11-293-697-3946
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21	167	4.6	864	7	US-11-312-797-2
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23	166	4.6	391	7	US-11-253-200-15
24	151.5	4.2	866	7	US-11-312-797-4
25	137.5	3.8	534	7	US-11-253-200-124

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Sequence 113, App
Sequence 6, Appli
Sequence 122, App
Sequence 3, Appli
Sequence 109, App
Sequence 92, Appl
Sequence 84, Appl
Sequence 100, App
Sequence 12, Appl
Sequence 11, Appl
Sequence 3942, Ap
Sequence 23, Appl
Sequence 5161, Ap
Sequence 4, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 772, App
Sequence 2959, Ap

3.8 373 7 US-11-253-200-9
3.7 279 7 US-11-253-200-113
3.7 376 7 US-11-253-200-6
3.7 414 7 US-11-253-200-122
3.7 454 7 US-11-253-200-3
3.6 414 7 US-11-253-200-109
3.6 351 7 US-11-253-200-92
3.6 429 7 US-11-253-200-84
3.6 636 7 US-11-253-200-102
3.6 714 7 US-11-253-200-100
3.6 510 7 US-11-253-200-12
3.4 533 7 US-11-253-200-11
3.4 390 7 US-11-293-697-3942
3.2 421 7 US-11-253-200-23
3.1 3575 7 US-11-330-403-5161
2.9 1237 7 US-11-045-540-4
2.9 1248 7 US-11-045-540-5
2.9 964 6 US-10-142-275B-2
2.8 3020 7 US-11-140-487A-772
2.7 354 7 US-11-293-697-2959

ALIGNMENTS

RESULT 1

US-10-196-749-598

; Sequence 598, Application US/10196749

; Publication No. US20060094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC340

; CURRENT APPLICATION NUMBER: US/10/196,749

; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 598

; LENGTH: 705

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-196-749-598

Db 480 GWRLKQDVRSAAARG-RAALLYSADDSGFERLVGALASALCOLPVRVAVDLWSRRE 538
 Qy 514 LSAHGALAFWHQRRRIIQEGGWILLFSPAQAQOQWLQQTVEP---GPHDALAAWL 570
 Db 539 LSAQGPVAFWFAQRQTQEGGVVLLFSPGVALCSEWLQDGVSGPGAHGPHDAFRASL 598
 Qy 571 SCVLPDFLQGRATGRYGVYFDGLLHPDSVPSPRPAFLPSLPTQLPAFLDALQGCST 630
 Db 599 SCVLPDFLQGRAPSGYVACFDRLLHPDAVPALFRTVFTLPSQLPDFLQALQOPR 658
 Qy 631 AGRPADRVERTQALRSALDSC--TSSSEAPG 660
 Db 659 SGRQERAEQVSRALQALPDLSYFHPGTPAG 690

RESULT 3

US-11-311-561-14
 ; Sequence 14, Application US/11311561
 ; Publication No. US2006008917A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: VanLookeren, Menno
 ; APPLICANT: Vandlen, Richard
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William
 ; APPLICANT: Yansura, Daniel
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C1P1 US/11/311,561
 ; CURRENT APPLICATION NUMBER: US/11/311,561
 ; PRIOR FILING DATE: 2005-12-20
 ; PRIOR APPLICATION NUMBER: US/09/747,259
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/172,096
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/31274
 ; PRIOR FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: US 60/175,481
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 60/191,007
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/07532
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 39

SEQ ID NO 14
 ; LENGTH: 705
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-11-311-561-14
 Query Match 64.9%; Score 2339; DB 7; Length 705;
 Best Local Similarity 66.3%; Pred. No. 4.7e-198;
 Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;

Qy 1 MPVSWFLSLAIGRNPVVVSLRLMBPQDARTARCSLGLSCHLWDGDLVCLPGSLQSPGPV 60
 Db 1 MPVSWFLSLAIGRNPVVVSLRLMBPQDARTARCSLGLSCHLWDGDLVCLPGSLQSPGPV 60
 Qy 61 LVPTRLQTLVLRCKQKTDCLARVVRVHLAVHGHWAPEE-----AGKSSESEIQESNAS 116
 Db 61 LAPTHLQTLVLRCKQKTDCLARVVRVHLAVHGHWAPEE-----AGKSSESEIQESNAS 120
 Qy 117 LQAQVVLSPQAPIARCALLEVQVPADLVQPGSVGSNAFDCFEASIGARVQIWSYTKPR 176
 Db 121 LQAQVVLSPQAPIARCALLEVQVPADLVQPGSVGSNAFDCFEASIGARVQIWSYTKPR 180
 Qy 177 YQELNLITQOLP-----DGDNVLLTLDVSEEQDFSLLYLRVPVDPALKSLWYKNLT 227
 Db 181 YQELNLITQOLP-----DGDNVLLTLDVSEEQDFSLLYLRVPVDPALKSLWYKNLT 240
 Qy 228 GPQNTLNHTDLVPCLCIQVMSLEPDSERVEPCPFREDPGAHNLWHIARLRLVSPGVWQ 287
 Db 241 GPQNTLNHTDLVPCLCIQVMSLEPDSERVEPCPFREDPGAHNLWHIARLRLVSPGVWQ 300
 Qy 288 LDAPCCLPGKVTLCWQAPDQSPQPLVPPVQKNATVNEPQDFQLVAGHPNLCVQVSTWE 347
 Db 301 LDAPCCLPGKVTLCWQAPDQSPQPLVPPVQKNATVNEPQDFQLVAGHPNLCVQVSTWE 360
 Qy 348 KYQLQACSWADSLGPFKDDMLVEMKTLNNTSVCALEPGCTPLPSMASTRARLGEEL 407
 Db 361 KYQLQACSWADSLGPFKDDMLVEMKTLNNTSVCALEPGCTPLPSMASTRARLGEEL 420
 Qy 408 LQDFRSHOCWLNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALPFFLLKKDRRK 467
 Db 421 LQDFRSHOCWLNDDNMGSLWACPMCKYIHRRWLVWLACLLAAALPFFLLKKDRRK 479
 Qy 468 -----AAGSRRTALLHSADGAGYERLVGALASALSQMPLRVAVDLWSRRE 513
 Db 480 GWRLKQDVRSAAARG-RAALLYSADDSGFERLVGALASALCOLPVRVAVDLWSRRE 538
 Qy 514 LSAHGALAFWHQRRRIIQEGGWILLFSPAQAQOQWLQQTVEP---GPHDALAAWL 570
 Db 539 LSAQGPVAFWFAQRQTQEGGVVLLFSPGVALCSEWLQDGVSGPGAHGPHDAFRASL 598
 Qy 571 SCVLPDFLQGRATGRYGVYFDGLLHPDSVPSPRPAFLPSLPTQLPAFLDALQGCST 630
 Db 599 SCVLPDFLQGRAPSGYVACFDRLLHPDAVPALFRTVFTLPSQLPDFLQALQOPR 658
 Qy 631 AGRPADRVERTQALRSALDSC--TSSSEAPG 660
 Db 659 SGRQERAEQVSRALQALPDLSYFHPGTPAG 690

RESULT 4

US-11-101-316-162
 ; Sequence 162, Application US/11101316
 ; Publication No. US2006009657A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
 ; FILE REFERENCE: P3230R1C17C1
 ; CURRENT APPLICATION NUMBER: US/11/101,316
 ; CURRENT FILING DATE: 2005-04-06
 ; PRIOR APPLICATION NUMBER: 10/063526
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: 10/006867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 09/380137
 ; PRIOR FILING DATE: 1999-08-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252

;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 170
;; SEQ ID NO 162
;; LENGTH: 705
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-11-101-316-162

Query Match 64.9%; Score 2339; DB 7; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;
Qy 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVLCLPGSLQSPGV 60
Db 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVLCLPGSLQSPGV 60
Qy 61 LVPTRLOTELVLRCPOKTDCCALRVVVVHLAVHGHWAEP-AGKSDSELQESRNAS 116
Db 61 LAPTHLOTELVLRCQKTDCCALRVVVVHLAVHGHWAEPDEEKEFGGAADSGVEEPN 120
Qy 117 LQAQVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCFEASLGAQVQIWSYTKPR 176
Db 121 LQAQVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCFEASLGAQVQIWSYTKPR 180
Qy 177 YQKELNLTQQLP-----DGDNVLLTLTVSEEQDFSLFLYLRVPDALKSLWKYKNT 227
Db 181 YQKELNLTQQLPALPWLNVSDGDNVHLVNVSEHQFGLSLYWNQVQPPKPRWHKNT 240
Qy 228 GPQNTITLNTDILVPCLCIQVMSLEPDSERVEFCPPREDPFAHNLWHIARLVLSPGVNQ 287
Db 241 GPQNTITLNTDILVPCLCIQVMSLEPDSERVEFCPPREDPFAHNLWHIARLVLSPGVNQ 300
Qy 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPOKNAITNEPQDFQVAGHPNLCVQVSTWE 347
Db 301 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPOKNAITNEPQDFQVAGHPNLCVQVSTWE 360
Qy 348 KVQLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEEL 407
Db 361 KVQLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEEL 420
Qy 408 LQDFRSHQCMQWDDNMGSLWACPMCKYIHRVWVWLA CLLLAAALFFFLILKKDRK 467
Db 421 LQDLQSGQCLQW-DDDGLGALWACPMCKYIHKRWALVWLA CLLLAAALFFFLILKKDRK 479
Qy 468 -----AARGSRALLHSADGAGYERLVGALASALSOMPLRVAVDLWSRRE 513
Db 480 GWBLRLKQDVRSQAARG-RAALLLYSADDSGFELVGLASALCOLPLRVAVDLWSRRE 538
Qy 514 LSAHGALAWFHQRRIILQEGGVVILLFSPAQAQCOOWLOQTVEP---GPHDALAAWL 570
Db 539 LSAQGVAVFHAQRRTLOEGGVVLLFSPGAVALCSEWLQDGVSGPAGHGFHDAFRASL 598
Qy 571 SCVLPDFLOGRATGRYGVYFDGLLHPDSVSPRVAFLPSLTQPLPAFLDALQGGCSTS 630
Db 599 SCVLPDFLOGRATGRYGVYFDGLLHPDSVSPRVAFLPSLTQPLPAFLDALQGGCSTS 658
Qy 631 AGRPADRVETQALRSALDSC--TSSEAPG 660
Db 659 SGRLQERAEQVSRALQALDLSYFHPGTPAG 690

RESULT 5
US-11-311-554-14
;; Sequence 14, Application US/11311554
;; Publication No. US20060134755A1
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Tumas, Daniel
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: P1381R1CPI(US)
;; CURRENT APPLICATION NUMBER: US/11/311,554
;; CURRENT FILING DATE: 2005-12-20
;; PRIOR APPLICATION NUMBER: US/09/747,259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US 09/311,832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/172,096
;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: PCT/US99/31274
;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: US 60/175,481
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: US 60/191,007
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: PCT/US00/07532
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 14
;; LENGTH: 705
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-11-311-554-14

Query Match 64.9%; Score 2339; DB 7; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;
Qy 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVLCLPGSLQSPGV 60
Db 1 MPVSWFLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGVLCLPGSLQSPGV 60
Qy 61 LVPTRLOTELVLRCPOKTDCCALRVVVVHLAVHGHWAEP-AGKSDSELQESRNAS 116
Db 61 LAPTHLOTELVLRCQKTDCCALRVVVVHLAVHGHWAEPDEEKEFGGAADSGVEEPN 120
Qy 117 LQAQVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCFEASLGAQVQIWSYTKPR 176
Db 121 LQAQVLSFQAYPIARCALLEVQVPADLVQPGQSGVSAVDFCFEASLGAQVQIWSYTKPR 180
Qy 177 YQKELNLTQQLP-----DGDNVLLTLTVSEEQDFSLFLYLRVPDALKSLWKYKNT 227
Db 181 YQKELNLTQQLPALPWLNVSDGDNVHLVNVSEHQFGLSLYWNQVQPPKPRWHKNT 240
Qy 228 GPQNTITLNTDILVPCLCIQVMSLEPDSERVEFCPPREDPFAHNLWHIARLVLSPGVNQ 287
Db 241 GPQNTITLNTDILVPCLCIQVMSLEPDSERVEFCPPREDPFAHNLWHIARLVLSPGVNQ 300
Qy 288 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPOKNAITNEPQDFQVAGHPNLCVQVSTWE 347
Db 301 LDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPOKNAITNEPQDFQVAGHPNLCVQVSTWE 360
Qy 348 KVQLQACSWADSLGPFKDDMLLVEMKTLGNTSVCALEPSCGCTPLPSMASTRARLGEEL 407

Db 361 KQQLQECWADSLGKPLKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
Qy 408 LQDFRSQCHQWLDNDNGSLWACPMCKYIHRVWLVWLACLLAAALFFFLLLKDDRRK 467
Db 421 LQDLQSGQCLQW-DDDLGALWACPMCKYIHKRWLVWLACLLFAAALLSLLLKKDHAK 479
Qy 468 -----AARGSRFALLHSGADGAGYERLVGALASALSOMPLRVAVDLWSRRE 513
Db 480 GWRLLKQDVRSGAAARG-RAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRE 538
Qy 514 LSAHGAALWAFHQRRILOEGGVVILLFSPAQAQCOOVLQOTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFHQAQRQTLQEGGVVILLFSPGAVALLCSEWLDQGVSGGAGPHDAFRASL 598
Qy 571 SCVLPDFLOGRATGRYGVYFDGLLHSDSPSPFRVAPLFLSLTQLPALFALDQGCST 630
Db 599 SCVLPDFLOGRAPGSYGVACFDRLHDPDAVPALFRTVPVFTLPSQDFLQALQOPR 658
Qy 631 AGRPDRVVRTQALRSALDSC--TSSSEAPG 660
Db 659 SGRLOERAEQVSRALQALDYSYFHPGTPAPG 690
RESULT 6
US-11-376-673-162
; Sequence 162, Application US/11376673
; Publication No. US20060160186A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
; TITLE OF INVENTION: LUNG TUMOR
; FILE REFERENCE: P3230R1C165C
; CURRENT APPLICATION NUMBER: US/11/376,673
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/063742
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-376-673-162

Query Match 64.9%; Score 2339; DB 7; Length 705;
Best Local Similarity 66.3%; Pred. No. 4.7e-198;
Matches 459; Conservative 66; Mismatches 133; Indels 34; Gaps 7;
Qy 1 MPVSWFLLSALGHNVPVLSERLWBPQDTCARCSLGLSCHLWDGDLVLCPSLQASAPGV 60
Db 1 MPVSWFLLSALGHNVPVLSERLWBPQDTCARCSLGLSCHLWDGDLVLCPSLQASAPGV 60
Qy 61 LVPTLQTLVLRCPQKTCDCALVRVVVHLAVHGHWAEPB-----AGKSDSELOESRNAS 116
Db 61 LAPTHLQTLVLRCPQKTCDCALVRVVVHLAVHGHWAEPB-----AGKSDSELOESRNAS 120
Qy 117 LQAVQLSFOAYPTARCALLEVQVADLVQPGQSVGSAVFCFASLCAEQVQISYTKPR 176
Db 121 LQAVQLSFOAYPTARCALLEVQVADLVQPGQSVGSAVFCFASLCAEQVQISYTKPR 180
Qy 177 YQKELNLTQLP-----DGDVLLTLNDSBEQDPFSLLYLRPVPDALKSLWYKNT 227
Db 181 YQKELNLTQLP-----DGDVLLTLNDSBEQDPFSLLYLRPVPDALKSLWYKNT 240

Qy 228 GPQNTTLNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAHRNLWHIARLRLVLSGCVWQ 287
Db 241 GPQNTTLNHTDLVPCLCIQVMSLEPDSERVEFCPPREDPGAHRNLWHIARLRLVLSGCVWQ 300
Qy 288 LDAPCCLPGKVTLCQWADPQSPQPLVPPVPKRNATVNEPQDFQVAGHPNLCVQVSTWE 347
Db 301 LDAPCCLPAEALCWRAPGDPCQPLVPPPLSWENVTVDKVLBPPLKHPNLCVQVNSSE 360
Qy 348 KVQLQACSWADSLGPPKDDMLLVEMKTYGLNNTSVCALEPSCGCTPLPSMASTRARLGEEL 407
Db 361 KQLQCEQLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAARLGEYL 420
Qy 408 LQDFRSQCHQWLDNDNGSLWACPMCKYIHRVWLVWLACLLAAALFFFLLLKDDRRK 467
Db 421 LQDLQSGQCLQW-DDDLGALWACPMCKYIHKRWLVWLACLLFAAALLSLLLKKDHAK 479
Qy 468 -----AARGSRFALLHSGADGAGYERLVGALASALSOMPLRVAVDLWSRRE 513
Db 480 GWRLLKQDVRSGAAARG-RAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRE 538
Qy 514 LSAHGAALWAFHQRRILOEGGVVILLFSPAQAQCOOVLQOTVEP---GPHDALAAWL 570
Db 539 LSAQGPVAFHQAQRQTLQEGGVVILLFSPGAVALLCSEWLDQGVSGGAGPHDAFRASL 598
Qy 571 SCVLPDFLOGRATGRYGVYFDGLLHSDSPSPFRVAPLFLSLTQLPALFALDQGCST 630
Db 599 SCVLPDFLOGRAPGSYGVACFDRLHDPDAVPALFRTVPVFTLPSQDFLQALQOPR 658
Qy 631 AGRPDRVVRTQALRSALDSC--TSSSEAPG 660
Db 659 SGRLOERAEQVSRALQALDYSYFHPGTPAPG 690
RESULT 7
US-11-293-697-2756
; Sequence 2756, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2756
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2756

Query Match 30.1%; Score 1086; DB 7; Length 343;
Best Local Similarity 67.0%; Pred. No. 7.4e-88;
Matches 217; Conservative 35; Mismatches 66; Indels 6; Gaps 3;
Qy 342 QVSTWERYQLOACSWADSLGPPKDDMLLVEMKTYGLNNTSVCALEPSCGCTPLPSMASTRAA 401
Db 6 QVNSEKQLQCEQLWADSLGPKDDVLLLETRGPQDNRSICALPESGCTSLPSKASTRAA 65
Qy 402 RLGEELLQDFRSQCHQWLDNDNGSLWACPMCKYIHRVWLVWLACLLAAALFFFLLL 461
Db 66 RLGEYLLQDLQSGQCLQW-DDDLGALWACPMCKYIHKRWLVWLACLLFAAALLSLLL 124
Qy 462 KDDRRKKAARGSRFALLHSGADGAGYERLVGALASALSOMPLRVAVDLWSRRELSAHGALA 521
Db 125 KDDHKAARGAALLYSADDSGFERLVGALASALCOLPLRVAVDLWSRRELSAQGPVA 184
Qy 522 WFHQRRILOEGGVVILLFSPAQAQCOOVLQOTVEP---GPHDALAAWLSCVLPDFL 578
Db 185 WFHQRRILOEGGVVILLFSPAQAQCOOVLQOTVEP---GPHDALAAWLSCVLPDFL 244

QY 579 QGRATGRVGVYFDGLHPSVPSFRRVAPLFSIPTQLPAFLDALOGGCSSTAGRPADRV 638
Db 245 QGRAPGSVVGACFDRLHPSVPSFRRVAPLFSIPTQLPAFLDALOGGCSSTAGRPADRV 304
QY 639 ERVTQALRSALDSC--TSSSEAPG 660
Db 305 EQVSRALQPALDSYFHPGCTPAPG 328

RESULT 8

US-11-293-697-3960
; Sequence 3960, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3960
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3960

Query Match 20.5%; Score 739; DB 7; Length 261;
Best Local Similarity 63.2%; Pred. No. 2.2e-57;
Matches 156; Conservative 22; Mismatches 49; Indels 20; Gaps 4;

QY 433 MDKVIHRRVWLVLACLLAALFFLLKKDKRK-----AARGSRATALL 478
Db 1 MDKVIHRRVWLVLACLLAALFFLLKKDKRK-----AARGSRATALL 59
QY 479 HSADGAGVERLVGALASALSMPLRVAVDLWSRRELSAHGALWPHHRRILQEGGVI 538
Db 60 YSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFHQAORRTLQEGGVV 119
QY 539 LFSPPAAVQCOOVLQOTVEP---GPHDALAAMLSVLPDFLOGRATGRVGVYFDGLL 595
Db 120 LFSPPAAVQCOOVLQOTVEP---GPHDALAAMLSVLPDFLOGRATGRVGVYFDGLL 179
QY 596 HPDSVPSFRRVAPLFSIPTQLPAFLDALOGGCSSTAGRPADRVVTOALRSALDSC--T 653
Db 180 HPDAVPAFLFRVPTVFTLPSQLPDLFGALQOPRAPRSGRLQERAEQVSRALQPALDSYFHP 239
QY 654 SSSSEAPG 660
Db 240 PGTPAPG 246

RESULT 9

US-11-253-200-14
; Sequence 14, Application US/11253200
; Publication No. US20060142192A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Appleby, Mark W.
; APPLICANT: Lewis, Katherine E.
; APPLICANT: McKernan, Patricia A.
; APPLICANT: Okada, Shannon L.
; APPLICANT: Taft, David W.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Levin, Steven D.
; TITLE OF INVENTION: SOLUBLE ZCYTOR21, ANTI-ZCYTOR21
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION

; FILE REFERENCE: 04-13
; CURRENT APPLICATION NUMBER: US/11/253,200
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 60/619,651
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/622,207
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-253-200-14

Query Match 9.4%; Score 338.5; DB 7; Length 637;

Best Local Similarity 27.5%; Pred. No. 1.8e-21;
Matches 131; Conservative 56; Mismatches 22; Indels 67; Gaps 18;
QY 224 KMLTGPQNTLNTHTDLVPCLCIQWWSLEPDSERVFECFPREDPGAH-RNLWHIARLRVLS 282
Db 183 KIVSGGHTVDLPYEFLLPCMIEASYLOEDTVRRKKCPQSWPEAYGDFWQSIREFTDYS 242
QY 283 PG---VWOLDAPCCLPKGVTLWCQAPDOSPCOPLVPPVPQKNATVNEPODFOLVAG---H 336
Db 243 QHNQVMALTLRCPLKLEASLCWRQDPLTPCETL-----PNATAQESGWIENVDLH 296
QY 337 PNLGVQSVTWKVLQOAC-----SWADSLGPPFKDDMLLVEMKTLGLNNTSVCALEPSG 388
Db 297 PQLCFKFS-FENSSHVECPHQSGSLPSTVMDT-QAQLTLHFSSRTVATFSAAWSDFG 354
QY 399 C---TPLEPSMASTRARLGEELLQD-----FRSHOCMLNDDNMGSLW---ACPMDKYI 437
Db 355 LGPDTMPMPVYSISOTQGSVPVTLIIIPFLRQENCILVWRSRSD-VHFAWKHVLCP--DVS 411
QY 438 HRRVWLVLACLLAALFFLLKKDKRKKAARG-SRTALLHLSADGAGYERLVGALASA 496
Db 412 HRHGLGLTLALALATLVGVVLLVLRLLPGSGRTRPVLLHLLHAADSEARQLRVGALAE 471
QY 497 LSQM---PLRVAVDLWSRRELSAHGALWPHHRRILQEGGVILLFSPAAVQCOOVL 553
Db 472 LRTALGGGRDVIDLWEGTHVARIGPLPWLMAAREVAREQGTVLLLMNCAGFS----- 525
QY 554 QLQTVPECPHDAALWLSVLPDFLOGRATGRVGVYFDGLHPSVPSFRRVAPLFSLP 613
Db 526 --TACSGDPQASRLTLCAAPRPL-----LLAYFSRLCAKGDIPRLPLPRYRL 575
QY 614 TQLPAFLDALOGGCSSTA-----GRPADRVVTOA-----LRSALDSCSSSEAP 659
Db 576 RDLPRLLRALDAQPATLASSWSHLGAKRCLNRLKLEQCHLLEAAKDDYQGSTNSP 631

RESULT 10

US-11-253-200-111
; Sequence 111, Application US/11253200
; Publication No. US20060142192A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Appleby, Mark W.
; APPLICANT: Lewis, Katherine E.
; APPLICANT: McKernan, Patricia A.
; APPLICANT: Okada, Shannon L.
; APPLICANT: Taft, David W.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Levin, Steven D.
; TITLE OF INVENTION: SOLUBLE ZCYTOR21, ANTI-ZCYTOR21
; TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-13
; CURRENT APPLICATION NUMBER: US/11/253,200
; CURRENT FILING DATE: 2005-10-18

us-10-719-202-2.rapbn

Tue Aug 22 11:34:38 2006

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; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/11/311,555
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-11-311-555-16

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Query Match 8.6%; Score 310; DB 7; Length 667;
Best Local Similarity 28.1%; Pred. No. 6.3e-19;
Matches 130; Conservative 56; Mismatches 214; Indels 62; Gaps 18;

QY 224 KNLGTGPNITLHNTDLPCLCIQVMSLEPDSERVFCEPREDPCGAH-RNLW---HIARLR 279
DB 223 KIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYS 282
QY 280 VLSPGVQWLDAPCCLPGKVTLCWQAPDQSPQPLVPPVPOKNATVNEPQDF---QLVAGH 336
DB 283 QHTQMWALTLCPLKLEAALCORHWTLCCKL-----PNATARESDBGWVLEKVDLH 336
QY 337 PNLGVQVSTWVKVQLQA-----CSWADSLGPPKDDMLLVEMKTLNNTSVCALEPSGC 389
DB 337 PQLCFKFSFGNSHVECHPQTSGLTSMNVSMPT-QAQLILHFSRMRHATFSAWSLPLGL 395
QY 390 ---TLPSPMASTRAARLGBELLQD-----FRSHQCHQWLNDDNMGLW---ACPMKDYIH 438
DB 396 GQDTLVPPVTVSQARGSSPVSLDLIIPFLRPGCCVLRWSD-VQFAMKHLCPDVSYRH 454
QY 439 RRWLVWMLACLLAAALPFFLLKKDRKAARG-SRTALLLHSDAGAGYERLVGALASAL 497
DB 455 LG--LLILALLALTLLGVVLTCTCRPQSGFPGPARPVLLHRAADSEARQLVGALELL 512
QY 498 SOM---PLRVAVDLWSRRELSSAHGALAWFHQRRIILQEGGVVILLFSPAQAQCOQWLQ 554
DB 513 RAALGGGRDVIIDLMEGRHVARVGLPWLMAARTVAREQGTVLLWSGA-----D 563
QY 555 LQTVPEPGHDALAAWLSVLPDFLQGRATGRYGVYFDGLLHSDVSPSPFRVAPLFLSLPT 614
DB 564 LRPVS-GPDPRAPPLA-----LHAAPRPLLILAYSRCLCAKGDIPPLRALPRYELLR 617
QY 615 QLPAPFLDALQ---GCSTAGRPADRVERTVQALRSALDSCT 653
DB 618 DLPRLLRALDARPPAATSWGRIGARQRR-----QSRLELCS 654

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Search completed: August 16, 2006, 11:51:40
Job time : 36 secs

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; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 04-13
; CURRENT APPLICATION NUMBER: US/11/253,200
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 60/619,651
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/622,207
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-253-200-107

Query Match 8.6%; Score 310; DB 7; Length 650;
Best Local Similarity 28.1%; Pred. No. 6.1e-19;
Matches 130; Conservative 56; Mismatches 214; Indels 62; Gaps 18;

QY 224 KNLGTGPNITLHNTDLPCLCIQVMSLEPDSERVFCEPREDPCGAH-RNLW---HIARLR 279
DB 206 KIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYS 265
QY 280 VLSPGVQWLDAPCCLPGKVTLCWQAPDQSPQPLVPPVPOKNATVNEPQDF---QLVAGH 336
DB 266 QHTQMWALTLCPLKLEAALCORHWTLCCKL-----PNATARESDBGWVLEKVDLH 319
QY 337 PNLGVQVSTWVKVQLQA-----CSWADSLGPPKDDMLLVEMKTLNNTSVCALEPSGC 389
DB 320 PQLCFKFSFGNSHVECHPQTSGLTSMNVSMPT-QAQLILHFSRMRHATFSAWSLPLGL 378
QY 390 ---TLPSPMASTRAARLGBELLQD-----FRSHQCHQWLNDDNMGLW---ACPMKDYIH 438
DB 379 GQDTLVPPVTVSQARGSSPVSLDLIIPFLRPGCCVLRWSD-VQFAMKHLCPDVSYRH 437
QY 439 RRWLVWMLACLLAAALPFFLLKKDRKAARG-SRTALLLHSDAGAGYERLVGALASAL 497
DB 438 LG--LLILALLALTLLGVVLTCTCRPQSGFPGPARPVLLHRAADSEARQLVGALELL 495
QY 498 SOM---PLRVAVDLWSRRELSSAHGALAWFHQRRIILQEGGVVILLFSPAQAQCOQWLQ 554
DB 496 RAALGGGRDVIIDLMEGRHVARVGLPWLMAARTVAREQGTVLLWSGA-----D 546
QY 555 LQTVPEPGHDALAAWLSVLPDFLQGRATGRYGVYFDGLLHSDVSPSPFRVAPLFLSLPT 614
DB 547 LRPVS-GPDPRAPPLA-----LHAAPRPLLILAYSRCLCAKGDIPPLRALPRYELLR 600
QY 615 QLPAPFLDALQ---GCSTAGRPADRVERTVQALRSALDSCT 653
DB 601 DLPRLLRALDARPPAATSWGRIGARQRR-----QSRLELCS 657

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RESULT 15

US-11-311-555-16
Sequence 16, Application US/11311555
Publication No. US2006008916A1

```

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P Mickey

```
